



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143685

TO: Ruixiang Li
Location: rem/4d75/4c70
Art Unit: 1646
Monday, February 14, 2005

Case Serial Number: 10/689832

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib

143 685

mg

From: Li, Ruixiang
Sent: Sunday, January 30, 2005 2:05 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/689,832

RECEIVED
JAN 31 2005
(STIC)

Please do a standard search on:

- (i). SEQ ID NOS: 19 and 20 against commercial nucleic acid databases;
- (ii). SEQ ID NO: 20 against commercial amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 2/8/05
Date Completed: 2/14/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search 1
NA Sequence: # _____
AA Sequence: # 1+1 - reverse to MA
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: QSP
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:30:01 ; Search time 3513 Seconds
(without alignments)
12124.656 Million cell updates/sec

Title: US-10-689-832-19
Perfect score: 1119
Sequence: 1 atggagcacacgcagccca.....cttgtgtcatcatctgtga 1119

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	457.8	40.9	803	9	CC905917 t025011ba
C 2	250	22.3	362	8	AZ513631 1M0359L07
C 3	229.4	20.5	448	8	AQ225693 HS 2009.B
C 4	218.8	19.6	813	8	BZ189352 CH230-259
C 5	209.8	18.7	806	9	CNS02284 AL178069 Tetradon
C 6	200	17.9	588	8	AQ344035 RPC111-12
C 7	197	17.6	603	8	AQ351433 CL137737 ISB1-110A
C 8	183	16.4	824	9	CL137737 ISB1-110A
C 9	182.8	16.3	947	9	CNS02BVO AL190367 Tetradon
C 10	173	15.5	708	5	BU610327 UT-M-DJ2
C 11	169.4	15.1	1289	9	CL649540 CH213-237
C 12	150	13.4	867	9	CL137848 ISB1-110C
C 13	149	13.3	898	9	CNS02ENP AL193966 Tetradon
C 14	111.8	10.0	1107	9	CNS04L7F AL295764 Tetradon
C 15	111	9.9	515	1	AL921815 AL921815
C 16	87.6	7.8	816	8	AZ535744 ENTC025TR
C 17	81.6	7.3	891	8	AZ683582 ENTK47TR
C 18	81.6	7.3	906	8	BH153606 ENTV583TF
C 19	77.8	7.0	843	8	AZ551618 ENTV54TR
C 20	77.4	6.9	908	8	AZ548467 ENTK30TR
C 21	75	6.7	850	8	BH146886 ENTPK48TF
C 22	71.8	6.4	900	8	AZ549980 ENTD94TF
C 23	71	6.3	976	8	BH149983 ENTD93TF
C 24	70.2	6.3	358	2	BB870915 BB870915

25	69.2	6.2	877	8	AZ531291	AZ531291	ENTBQ34TR
26	69.2	6.2	912	8	AZ551092	AZ551092	ENTFJ22TF
C 27	68	6.1	849	8	AZ546009	AZ546009	ENTFM53TF
28	67.8	6.1	488	9	FR0012324	FR0012324	AL003576 F.rubripe
29	67.6	6.0	888	8	AZ528430	AZ528430	ENTCO24TR
30	67	6.0	905	8	AZ550256	AZ550256	ENTEV58TR
31	66.2	5.9	721	5	BW141179	BW141179	BW141179
C 32	66	5.9	931	8	BH160272	BH160272	ENTQV49TR
C 33	63.6	5.7	890	8	AZ530768	AZ530768	ENTBH54TF
C 34	61.8	5.5	774	9	CNS02APC	AL188841	Tetradon
C 35	61.8	5.5	881	7	CNS97894	CNS97894	TTE000070
C 36	61.4	5.5	607	4	BJ348812	BJ348812	BJ348812
C 37	61.2	5.5	692	7	CR437869	CR437869	CR437869
C 38	61.2	5.5	726	7	CR438428	CR438428	CR438428
C 39	61.2	5.5	735	7	CR441503	CR441503	CR441503
C 40	61.2	5.5	768	7	CR445667	CR445667	CR445667
C 41	60.8	5.4	880	8	AZ529191	AZ529191	ENTBV68TR
C 42	60.8	5.4	954	7	CO250025	CO250025	AGENCOURT
C 43	60.6	5.4	712	7	CR438462	CR438462	CR438462
C 44	60	5.4	787	5	BW391073	BW391073	BW391073
45	60	5.4	1023	9	CNS05805	AL326174	Tetradon

ALIGNMENTS

RESULT 1
CC905917/c
LOCUS t025011ba.r1 TAMBT Bos taurus genomic clone t025011ba, genomic survey sequence.
DEFINITION CC905917
ACCESSION CC905917
VERSION CC905917.1 GI:33524850
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 803)
AUTHORS Lin, S., Najjar, F. Z., Adelson, D., Gill, C. A. and Roe, B. A.
TITLE Bovine BAC End Sequences from Library TAMBT
JOURNAL Unpublished (2003)
COMMENT Contact: Bruce A. Roe
Advanced Center for Genome Technology
University of Oklahoma Department of Chemistry and Biochemistry
620 Parrington Oval, Room 208, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Class: BAC ends
High quality sequence start: 39
High quality sequence stop: 551.
Location/Qualifiers
source 1..803
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Angus bull T A M U Shoshone Y6 11519666"
/db_xref="taxon:9913"
/clone="t025011ba"
/sex="Male"
/cell_type="Blood"
/clone_lib="TAMBT"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; TAMBT Bovine BAC library (Male) produced by Texas A&M University, Department of Animal Science."

ORIGIN

Query Match 40.9%; Score 457.8; DB 9; Length 803;
Best Local Similarity 88.9%; Pred. No. 2.2e-111;
Matches 506; Conservative 0; Mismatches 62; Indels 1; Gaps 1;
QY 483 CCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTATCAGCAC-CTCTGTGCATC 541

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2009 row: D column: 16
Class: BAC ends
High quality sequence stop: 448.

FEATURES
source

1. .448
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=2009 Col=16 Row=D"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: Sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 20.5%; Score 229.4; DB 8; Length 448;
Best Local Similarity 93.4%; Pred. No. 3.4e-50;
Matches 239; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 795 CATGTCGACATGCGCAACATGCTAGCCCTTCTGAACACAGCCATCAACTTCTTCTCTA 854
DB 445 CAGGTGAGCAATAGCAACAGTGTAGCCCTTGTGAGCAAGCCATCACTTCTTCTATA 386
QY 855 CTGCTTCATCAGCAAGCGGTTCCGACCAATGAGCGCGCCGACGCTCAAGGCTTCTTCAA 914
DB 385 CTGCGTTCATCAGCAAGCGGTTCCGACCAATGAGCGCGCCGACGCTCAAGGCTTCTTCAA 326
QY 915 GTGCCAGAGCAACCTGTACAGTCTTACACCATCATCACTTTTCCATACAGTAGCCCC 974
DB 325 GTGCCAGAGCAACCTGTACAGTCTTACACCATCATCACTTTTCCATACAGTAGCCCC 266
QY 975 CTGGATCTGCGCGGCAAACTCACATGTCATCAAGATGCTGGTGATCAGTATGACAAAA 1034
DB 265 CTGGATCTGCGCGGCAAACTCACATGTCATCAAGATGCTGGTGATCAGTATGACAAAA 206
QY 1035 TGGAAAACTTATAAA 1050
DB 205 TGGAAAACTTATAAA 190

RESULT 4

BZ169352
LOCUS CH230-259E22.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION CH230-259E22, genomic survey sequence.

ACCESSION BZ169352

VERSION BZ169352.1 GI:23810547

KEYWORDS GSS.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 813)

AUTHORS Zhao, S., Shetty, J., Shatsman, S., Teegave, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, P., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other_GSSs: CH230-259E22.TV

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/todb/bac_ends/rat/bac_end_intro.html
Plate: 259 row: E column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES
source

1. .813
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-259E22"
/sex="female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Query Match 19.6%; Score 218.8; DB 8; Length 813;
Best Local Similarity 86.7%; Pred. No. 2.8e-47;
Matches 241; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 125 CAGCAAAATCTTGACAGTGATCATCTCTCCAGCTGTGGCAAGACAGAAAGTCCT 184
DB 536 CAGCAAAATCTTGACAGTGATCATCTCTCACTGGTAGCAGACAGAAAGTCCT 595
QY 185 CCTCAACAATCTCTTGGCACTCGCTGCGCCGACATCTTGGTCTCTTTTCATAGTGT 244
DB 596 CCTCAACAATCTCTTGGCACTCGCTGCGCCGACATCTTGGTCTCTTTTCATAGTGT 655
QY 245 TTGTGACATCTCTTGTGGAAGATTTTCATCTTGAACATGACAGATGCTCAGGTCCCGACA 304
DB 656 TTGTGATTTCTTGTGGAAGATTTTCATCTTGAACATGACAGATGCTCAGGTCCCGACA 715
QY 305 AGATCATAGAAGTGTGGAATTTCTCATCCATCCACACCTCCATATGGATTTCTGTACCGT 364
DB 716 AGATCATAGAAGTGTGGAATTTCTCATCCATCCACACCTTTCTATTTGGATTACAGTCCCT 775
QY 365 TAACCATTTGACAGGTATATCGCTGCTGCCACCGCTC 402
DB 776 TAACCATTTGATAGGTATATCGCAGTCTGTCAACCCACTC 813

RESULT 5

CNS022E4
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 227D19 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION AL178069

VERSION AL178069.1 GI:7816126

KEYWORDS GSS; Genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1

AUTHORS Roest Crollius, H., Jaillon, O., Dagilva, C., Bouneau, L., Fisher, C.,

Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
2
Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
10899143
3 (bases 1 to 806)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1..806
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="227D19"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG227CB10LPI-end : T7"
ORIGIN
Query Match 18.7%; Score 209.8; DB 9; Length 806;
Best Local Similarity 56.3%; Pred. No. 7.4e-45;
Matches 418; Conservative 7; Mismatches 289; Indels 29; Gaps 1;
QY 166 GCAAGAAGACAGAAGTCTCTTACAACTATCTTTGGCACTCGCTGCGGACATCTTG 225
DB 2 GGAAGAAGACCAAGAGGGCTGTACTACTCTGCGGGGGTGACAGGCTCGGACATCTCTC 61
QY 226 GTCTCTTTTTCATAGTGTGTGGACTTCCTGTTGGAAGATTTTCATCTTGAACATGAG 285
DB 62 TCCAGCTCTTCATCATCTTCGTGGCTTCTCTGTTGGAGCGCGGTTTTCACCGGGAG 121
QY 286 ATGCCCTCAGGTCCCGACAGATCATAGAAGTGTGGAAATTCATCCATCCACACCTCC 345
DB 122 GTCCCGCGCTCTCTTACACTCAGTCAGCGCGCGCGAGTTTGGCGGCACACCGCTCC 181
QY 346 ATATGGATPACTGTACCGTTAACCAATTGACAGGTATATCGTGTCTGCCACCGCTCAAG 405
DB 182 ATCTGTCTCACGCTCCCTCACCGTGGACCGCTAGTGGCGCTGTGCCACCGCTCTCTC 241
QY 406 TACACACGGTCTCATACCCAGCGCGACCGGAAAGTCATTGTGAAGTGTTTACATCACC 465
DB 242 CACAGGCAGATCAGCTTACCGCGCGGACAGGAGGATCATCGCGTGTGTCTGTGTG 301
QY 466 TGTCTCTCAGCAGCATCCCTATTACTGTGTGCCCAACATCTGGACTGAAGACTACATC 525
DB 302 TGTGTGGCTCGGGCTCGCCCTTCTCTGTGTCCGATCGATGTGAGGAGACAGCACCGG 361
QY 526 AGCAGCTCTGTGCATCAGCTCTCTATCTGTGATCCACTGTCTCACCGTCTTACCTGGTGC 585
DB 362 CGGANGGGCTGAGCGCGTCTCTCATCTGGACCCAGTGAACCATCATCTACTTCTGTGCC 421
QY 586 TGTCTCATCTTTCTCATCTTGAATCATCATCTGTGTGTAACAGCTCAGGAGGAAGCAAT 645
DB 422 TGCAGCATCTTCTGTGTCTCAACTCTTTGATCATCCAMACGCTGAGGCTGCGGAGAG 481
QY 646 TTTCTGTCTCCGTGGCTACTCCAC-----GGGGNAGA 676

DB 482 CGGAGCGCGGGGGCGGCMCAAGTMCACGCTCCGCGCGCTGGGGAAGA 541
QY 677 CCACGGCATCTGTGTTCACCAATTACTCTCCATCTTTGGCACACTTTGGGCGCCCGGCATCA 736
DB 542 GCACGGCATCTGTGTGGCCATCACTCCGCTTCTGTGTCTGTGGGACCCAGGACGG 601
QY 737 TCATGATCTTTTACCACTCTATGGGGCGCCATCCAGACCGCTGGCTGGTGTACACATCA 796
DB 602 TGGTGGTCACTTACCACCTGTACGTTAGTGGTTCAACGGGAMTGGCGGCTCCACCTGG 661
QY 797 TGTCCGACATTTGCCAAACATGTAGCCCTTCTGAACACAGCCATCAACTTCTTCTCTACT 856
DB 662 CCTAGGACCTGTCCAAACATGCTGGCCATGCTCAACACGCGCGTAACTTCTTCTGTACT 721
QY 857 GCTTCATCAGCAAGCGGTTCCGC 879
DB 722 GCTTGTGTCAGCAAGCGGTTCCGC 744
RESULT 6
AQ344035/c
LOCUS
DEFINITION
RP111-124J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-124J23,
genomic survey sequence.
ACCESSION
AQ344035
VERSION
AQ344035.1 GI:4168931
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 588)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
JOURNAL
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbs@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: 17
Class: BAC ends.
Location/Qualifiers
1..588
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/db_xref="taxon:9606"
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/sex="Male"
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RPC111 Human Male BAC Library"
FEATURES
source
ORIGIN
Query Match 17.9%; Score 200; DB 8; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 CAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAGTCTCT 184

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Db      201 CAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAGTCTCT 142
Qy      185 CCTAACATATCTTTGGCACTGCTGCTCCGACATCTTGGTCTCTTTTTCATAGTGT 244
Db      141 CCTAACATATCTTTGGCACTGCTGCTCCGACATCTTGGTCTCTTTTTCATAGTGT 82
Qy      245 TTGTGACATCTCTTTGGAGATTTTCATCTTGAACATGACAGATGCTCAGGTCCCGACA 304
Db      81 TTGTGACATCTCTTTGGAGATTTTCATCTTGAACATGACAGATGCTCAGGTCCCGACA 22
Qy      305 AGATCATAGAGTGTGGAA 324
Db      21 AGATCATAGAGTGTGGAA 2

RESULT 7
AQ351433/c
LOCUS   AQ351433
DEFINITION RPCI11-113113.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-113113,
genomic survey sequence.
ACCESSION AQ351433
VERSION   AQ351433.1 GI:4178768
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 603)
AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL   Unpublished (1997)
COMMENT   Other GSSs: RPCI11-113113.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
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             /db_xref="taxon:9606"
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             /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
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ORIGIN
Query Match      17.6%; Score 197; DB 8; Length 603;
Best Local Similarity 100.0%; Pred. No. 1.8e-41;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      125 CAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAGTCTCT 184
Db      197 CAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAGTCTCT 138
Qy      185 CCTAACATATCTTTGGCACTGCTGCTCCGACATCTTGGTCTCTTTTTCATAGTGT 244


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Db      137 CCTAACATATCTTTGGCACTGCTGCTGGCAATCTTGGTCTCTTTTTCATAGTGT 78
Qy      245 TTGTGACATCTCTTTGGAGATTTTCATCTTGAACATGACAGATGCTCAGGTCCCGACA 304
Db      77 TTGTGACATCTCTTTGGAGATTTTCATCTTGAACATGACAGATGCTCAGGTCCCGACA 18
Qy      305 AGATCATAGAGTGTGCTG 321
Db      17 AGATCATAGAGTGTGCTG 1

RESULT 8
CLI37737
LOCUS   CLI37737
DEFINITION ISBI-110A2.T7.1 ISBI Xenopus tropicalis genomic clone ISBI-110A2,
genomic survey sequence.
ACCESSION CLI37737
VERSION   CLI37737.1 GI:40631372
KEYWORDS  Xenopus tropicalis (western clawed frog)
SOURCE    Xenopus tropicalis
ORGANISM  Xenopus tropicalis
REFERENCE 1 (bases 1 to 824)
AUTHORS   Krenitski,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
TITLE     A physical map of the xenopus tropicalis genome
JOURNAL   Unpublished (2003)
COMMENT   Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 2
High quality sequence stop: 672.
             Location/Qualifiers
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             /clone_lib="ISBI"
             /note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC
             Library Segment 1"

ORIGIN
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Best Local Similarity 59.5%; Pred. No. 1.2e-37;
Matches 309; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

Qy      125 CAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAGTCTCT 184
Db      167 CAGTGAACATGCTGACTGCTGTGGCACTCTCAAGGCTGGCATCGAGAACAAAGAGTCT 226
Qy      185 CCTAACATATCTTTGGCACTGCTGCTGGCACTCTTGGTCTCTTTTTCATAGTGT 244
Db      227 CCTACAGTTACCTGTTGGCTCTTACCATCTCGACATCTTGGCCAGATTTTTCATATTT 286
Qy      245 TTGTGACATCTCTTTGGAGATTTTCATCTTGAACATGACAGATGCTCAGGTCCCGACA 304
Db      287 TTGTGGGCTTTATCTCGCAACAGCAATACTCCACGGCAAGGTGCCAGTACCTTAATCC 346
Qy      305 AGATCATAGAGTGTGGAATTTCTCATCCATCCACCTCCATATGGATTACTGTACCGT 364
Db      347 ATGTGGTCAGTCTCTTGGATTTCTCTCTAAATCATGCATCTATTGGGTGACAGTGATAC 406
Qy      365 TAAACATTGACAGGTATATCGCTGTGCGACCCGCTCAAGTACACACAGGTCTCATACC 424
Db      407 TGACCGTGGACCGTTATGTGGCAATTATGCTATCCGCTACATATCGCTCTTTTCTTACC 466


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	Matches	257;	Conservative	3;	Mismatches	95;	Indels	9;	Gaps	1;
Qy	692	TCACCATTA	CTCCATCTTTGGCCACACTTTGGGCCCCCGGCATCATCATGATCTCTTTACC	751						
Db	7	TCGCCATCAGCTCCATTTTTCGGCTTCTGTGGGCGCGCACCTGATGATCTCTTACC	66							
Qy	752	ACCTCTATG	GGGGCGCCATCCAGAAACGGCT-----GGCTGGTACACATCATATGTCGG	802						
Db	67	ACTTCTACTCGCTTCGCCACGCTCGCGGGCGCGGGCGGCTCTGCACATTTCTCACCG	126							
Qy	803	ACATTGCCAACTAGTCAGCCCTTCTGAACACAGCCATCAACTTCTCTCTACTGCTTTCA	862							
Db	127	ATCTTGCCAACTATGTTGGCGTTGCTCAACAGGGTGTTAACTTCTTCTCTACTGTTTCA	186							
Qy	863	TCAGCAGCGGTTCCGCAACCATCGCAGCCCGCCAGCGCTCAAGGCTTTCTTCAAGTGCCAGA	922							
Db	187	TCAGCAGCGCTTTCCGGGGCATGGCGCCAACTGCTCGCAGCGCTGCTCCACTGCAGGA	246							
Qy	923	AGCAACCTGTACAGTTCTACACCAATCATAACTTTTCCATAACAAGTAGCCCTGGATCT	982							
Db	247	AGCAGCTGCAGCGGTTCTACGCCAGCCACAACATTTTCCATCACAGYTGCCCTGGWTCT	306							
Qy	983	CGCGGGCAAATCACA	CTGCATCAAGATGCTGGTGTACCAAGTATGCACAAAATGCGAAAC	1042						
Db	307	CACCAGCAAATCCCACTGCATCAAGATGCTGGTGTACCAAGTACGCACAAAACCGGGAAC	366							
Qy	1043	CTAT	1046							
Db	367	CCAT	370							

D5	187	1	CAGCAGACCGGTTCCGGGGGCAATGGCGGCGCAAGAGTGTCTCTGGAGGCGCTGCTCTCATCTGCAAGAA	241
Qy	923	AGCAACCTGTACAGTTCCTACACCAATCATAACTTTTCCATAACAAAGTAGGCCCTCGGATCT	982	
Db	247	AGCAGCTGCAGCGGTTCTAGCGCCAGGCCACAACATTTTCCATCAGCAGTGTGCCCTCGGWTCT	306	
Qy	983	CGCGGCAAACTCACACTGCATCAAGAGTCTGGTGTTACCAAGTATGCAGAAATCGGAAAC	1046	
Db	307	CACCAAGAAACTCCCACTGCATCAAGATGCTGGTGTACCAAGTACGACAAACCGGGAGC	366	
Qy	1043	CTAT	1046	
Db	367	CCAT	370	

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 708)
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	8889548 Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: m85t@mail.nih.gov Tissue Procurement: Dr. Robin Davison cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

FEATURES
source
1. .708
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"

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/db_xref="taxon:10090"
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/tissue_type="subfornical organ and postrema"
/dev_stage="Adult"

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/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
 /clone_lib="NIH_BMAP_DJ2"
 /notes="Organ: Brain; Vector: pTV73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-M-DJ2 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is: GCTACATGAT, subformal organ and area postrema."

ORIGIN

Query Match 15.5%; Score 173; DB 5; Length 708;
 Best Local Similarity 92.4%; Pred. No. 5.3e-35;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 854 ACTGCTTCATCAGCAAGCGGTCCGACCATGCGCGCCGCGCTCAAGGCTTTCTTCA 913
 DB 1 ACTGCTTCATCAGCAAGCGGTCCGACCATGCGCGCTCAAGGCTTTCTTCA 60

QY 914 AGTGCAGAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCATAACAAGTAGCC 973
 DB 61 AGTGTGAGAAGCAGCGCTGTACAGTTCTATACCAACCACTAACTTTTCATAACAAGTAGTC 120

QY 974 CTGGATCTCGCGGCAACTCAGCTGATCAAGATGCTGGTACCGATATGACAAA 1033
 DB 121 CTGGATCTCACCAGCAAACTCAGCTGATCAAGATGCTGGTACCGATATGACAAA 180

QY 1034 ATGGAACCTATAAAA 1050
 DB 181 ATGGAAGCCTATAAA 197

RESULT 11

LOCUS CL649540 1269 bp DNA linear GSS 06-JUL-2004
 DEFINITION CH213-237F13.SP6 CH213 Gasterosteus aculeatus genomic clone
 CH213-237F13 3', genomic survey sequence.

ACCESSION CL649540
 VERSION CL649540.1 GI:49668964

KEYWORDS GSS.

SOURCE Gasterosteus aculeatus (three spined stickleback)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.

1 (bases 1 to 1269)

REFERENCE Kingsley,D., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.

Expressed sequence tags from Gasterosteus aculeatus

Unpublished (2004)

CONTACT Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Avenue, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@shgc.stanford.edu

Plate: 237

Class: BAC ends

High quality sequence start: 19

High quality sequence stop: 869.

Location/Qualifiers

1..1269

/organism="Gasterosteus aculeatus"

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FEATURES

source

1..867

/organism="Xenopus tropicalis"

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/sex="Mixed"

/cell_type="Blood"

/clone_lib="CH213"

/note="Vector: pTARBAC2.1; Site 1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (http://cegs.stanford.edu). The clone was isolated from the BAC library CHORI-213 built by Pieter deJong in collaboration with the Stanford Genome Evolution Center (http://www.chori.org/bacpac/). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm)."

ORIGIN

Query Match 15.1%; Score 169.4; DB 9; Length 1269;
 Best Local Similarity 77.2%; Pred. No. 5.9e-34;
 Matches 206; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 777 CGCGTGGCTGTACATCATGTCCGACATTCGCAACATGCTAGCCCTTCTGAACACAGC 836
 DB 42 CGGGCGACTGCTCCAGGTGCTCACCGACCTGGCCATTATGCTCGCGTTGCTCAACACCGG 101

QY 837 CATCAACTTCTTCTTACTGCTTATCAGCAAGCGGTTCCGACCATGCGCAGCCGCCAC 896
 DB 102 GGTCAACTTCTTCTTACTGCTTATCAGCAAGCGGTTCCGCGGCATGCGCGCCCAACGT 161

QY 897 GCTCAAGGCTTCTTCAAGTGCAGCAAGCAACTGTGTACAGTTCTACACCAATCATACTT 956
 DB 162 CTGCGGGGCGCTGGTCACTGCGGGAAGCAGCGCGCGCTTCTACGCCAGCCACAACTT 221

QY 957 TTCCATAACAAGTAGCCCTCGATCTCGCGGCAAACTCACACTGTCATCAAGATGCTGGT 1016
 DB 222 TTCCATCACAAGCAGCGCGTGGATCTCACGCGCAACTCCCACTGCTTAAGATGCTGGT 281

QY 1017 GTACCAGTATGACAAAATGGAAAACC 1043
 DB 282 GTACCAGTATGACAAAATGGAAAACC 308

RESULT 12

LOCUS CL137848

DEFINITION

ISBI-110C15 T7.1 ISBI Xenopus tropicalis genomic clone ISBI-110C15, genomic survey sequence.

ACCESSION CL137848

VERSION CL137848.1 GI:40631483

KEYWORDS GSS.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM

Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 867)

REFERENCE Krenitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)

CONTACT: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@wustl.edu

Insert Length: 75000 Std Error: 0.00

Seq primer: T7 TAATACGACTCACTATAGG

Class: BAC ends

High quality sequence start: 11

High quality sequence stop: 673.

Location/Qualifiers

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Library Segment 1"
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Best Local Similarity 58.1%; Pred. No. 8.3e-29;
Matches 264; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 125 CAGCAATATCTTGACAGTATCATCTCCAGCTGTGGCAGAGACAGAGTCTT 184
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QY 185 CTTACAACTATCTTTGGCACTCGCTGCGGACATCTTGTCTCTTTTCATAGTGT 244
DB 242 CTTACAGTTACTGTGTGGCTCTTACCATCTCAGACATCTTGAGCCAGATTTTCATCATTT 301
QY 245 TTGTGGACTTCTGTGTGGAAGATTTTCATCTTGAACATGCAGATGCTCAGGTCCCGGACA 304
DB 302 TTGTGGGCTTTATCTCTGCAACAGCAATATCTCCAGCAAGGTGCCAGTACCTTAATCC 361
QY 305 AGATCATAGAAGTGTGGAATCTTCATCTCAGATCCATCCACACCTCCATATGGAATCTGTACCGT 364
DB 362 ATGTGGTCACTGTCTTGGATCTCTCTTAATCATGATCTATTTGGGTGACAGTGATAC 421
QY 365 TAACCATTCACAGGTATATCGTGTCTGCTGCCACCGCTCAAGTACCACAGGCTCTATACC 424
DB 422 TGACCGTGGACCGTGTATGGCATATGCTATCCGCTACAATATCGCTCTTTCTCTTACC 481
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DB 482 CAGAGCGAACCGTAGATCATTTGTCTTCTCTCATCTGTTGGACCGGTGTAC 541
QY 485 CTTATTAAGTGTGGCCCAACATCTGCACTGAAGATACATACAGCACCTCTGTGCATCAG 544
DB 542 CTTTCTACTGTGGAGTGTATTTGGAGGATCCGCTACCCAGGATGCTAGACCTTA 601
QY 545 TCCTCATCTGGATCCACCTGCTTCCACCGTCTACCT 578
DB 602 TACTCAAGTGGACCCACTCTTTATAATATACTT 635

RESULT 13
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LOCUS Tetraodon nigroviridis genome survey sequence PUC-ORI end of clone
DEFINITION 262F08 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL193966
VERSION AL193966.1 GI:7832072
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
2
Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
20359837
MEDLINE 10899143
PUBMED 3 (bases 1 to 898)
REFERENCE Direct Submission
AUTHORS Genoscope.
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Matches 292; Conservative 0; Mismatches 220; Indels 1; Gaps 1;
QY 121 TTACCAGCAATATCTTGACAGTATCATCTCTCCAGCTGTGGTGGCAAGACAGAG 180
DB 370 TTCCAGTGAACATCTTGACGCGGTGGCTTGACCCGCTGGCGTCCGCGACCAAGAG 429
QY 181 TCCTCTTACAATATCTCTTGCACTCTGCTGTCGCGACATCTTGGTCTCTTTTCATA 240
DB 430 GCACGTGTACTACTCTGCTGCGGTGACAGCTCCGACATCTCTCCAGCTCTTCATC 489
QY 241 GTGTTGTGGACTTCTCTGTGGAGATTTTCATCTTGAACATGCAGATGCCTCAGGTCCCC 300
DB 490 ATCTTCGTGGGCTTCTGTGGAGACGGCAGTTTTCACCGGAGGTCCCGCGCTCTC 549
QY 301 GACAAGATCATAGAAGTCTGGAATTTTCATCTCCATCCACACCTCCATATGGAATTA 360
DB 550 TTACACTCAGTCAGCGCGCGAGTTTGC CGCACCAACGCTCCATCTGGTCCACCGTC 609
QY 361 CGGTAAACATGACAGTATATCGCTCTGCGCACCGCTCAAGTACCAACAGCTCTCA 420
DB 610 CCCCTCACCGTGGACCGCTACGTGCGCTGTGCCACCCCTCTCCACAGGAGATCAGC 669
QY 421 TACCCAGCGCGCACCGGAAAGTCAATTGAAGTGTTCATCACCTGCTTCTGTGACCAGC 480
DB 670 TACCGCGCGCGCACAGGAGATCATCGCGGTGTCTGTGGTGTCTGCGTGGCCTCGG 729
QY 481 ATCCCTTATTAATCTGTTGGCCCAACATCTGGAATCTGAAGCTATACATCAGACCTCT 540
DB 730 CTGCGCTCTTCTTCTGTTGGTCCGACATGTGGAGGAACAGCCACC -CGCGACGSGTGA 788
QY 541 CAGTCTCTCATCTGGATCCATCTGCTTACCTTACCTGTTGGTGGCTCTGCTTCTTCTTC 600
DB 789 CGCGTCTCATCTGGACCCACGTGACCATCATCTACTTCTGCTGCGCTGAGCATCTTCTG 848
QY 601 ATCTTGAACCTCAATCATTTGTGTACAGCTCAGG 633
DB 849 GTCTTCAACTCTTTGATCATCTCCACGCTGAGG 881
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CNS04L7P
LOCUS Tetraodon nigroviridis genome survey sequence I7 end of clone
DEFINITION 118A07 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL295764
VERSION AL295764.1 GI:8034344

KEYWORDS
SOURCE GSS; genome survey sequence.
ORGANISM Tetraodon nigroviridis

REFERENCE
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Pizanes, C., Wincker, P., Brottier, P., Quetier, P., Saurin, W., and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645

REFERENCE
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Orzouf-Costaz, C., Pizanes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, P., Saurin, W., Bernot, A., and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143

REFERENCE
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 9106 EVRY cedex - FRANCE (E-mail : seqfr@genoscope.cns.fr)
JOURNAL - Web : www.genoscope.cns.fr

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
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Best Local Similarity 70.6%; Pred. No. 1.6e-18;
Matches 149; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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|||||
DB 70 GGGGAAGACACCGCCATCTGCTGGCCATCACCTCGCTTCTCTGTGCTCTGGGCACC 129
|||||

QY 729 CGGCATCATCATGATTTTACACCTCTATATGGGGGCCCATCCAGAACCGGTGGTGGT 788
DB 130 CAGGACGGTGGTGGTCACTTACCACCTGTACGTGCTGGTTCACCGGACCTGGCGCT 189
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QY 789 ACACATCATGTCGCATTCGCAACATGCTAGCCCTTCTGAACACAGCCATCACTTCTT 848
DB 190 CCACCTGGGCTAGCACTGTCCAAACATGCTGGCCTGATGCTCAACACGGCGTCACTTCTT 249
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QY 849 CCTTACTGCTTTCATCAGCAAGCGGTTCGGC 879
DB 250 CCTGTACTGCTTGTTCAGCAAGCGGTTCGGC 280
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RESULT 15
LOCUS AL921815
DEFINITION AL921815 PUR-21+22 Danio rerio cDNA clone 101-P03-2, mRNA sequence.
ACCESSION AL921815
VERSION AL921815.1 GI:23188395
KEYWORDS EST.

SOURCE
ORGANISM Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE
AUTHORS 1 (bases 1 to 515)
Lo, J., Lee, S., Xu, M., Liu, P., Ruan, H., Sun, A., He, Y., Ma, W., Wang, W., Wen, Z., and Peng, J.
TITLE 15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis
JOURNAL Genome Res. 13 (3), 455-466 (2003)
MEDLINE 22505427
PUBMED 12618376
COMMENT Contact: Peng J
Lab of Functional Genomics
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore, 117609, Singapore
Email: pengj@imcb.a-star.edu.sg
Clone requests: info@openbiosystems.com
Open Biosystems,
6705 Odyssey Drive, Huntsville, AL 35806.
FEATURES
source
1. .515
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Matches 190; Conservative 0; Mismatches 100; Indels 9; Gaps 1;

QY 640 AGCAATTTTCGCTCGTGGCTACTCCAGGGGAGACACCGCCATCTTTGCCACATT 699
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DB 214 AGCTGCTCCGGCTCGGAGGATCTGACCGGAAGACACCGGTATCTTTAGCATC 273
|||||

QY 700 ACCTCCATCTTTGCCACACTTTGGGCCCCCGCATCATCATGATTCTTTACCACTCTAT 759
|||||
DB 274 ACCTCAGTGTTCGGCTTTATGGGCGCTCGTACACTTATGATTCTTTATCATCTTTAC 333
|||||

QY 760 GGGGGCCCCATCCAGAACCGCTGGCTGG-----TACATCATGTCCGACATGCC 810
|||||
DB 334 ACGGTGCAACACGCGATGCCGGTCCGGCTAGACTCCTGCTATTTGGTAACGGATGTAGCG 393
|||||

QY 811 AACATGTAGCCCTTCTGAACACAGCCATCAACTTCTCTACTGCTTTCATCACAAG 870
|||||
DB 394 AACATGTTGCTTCTACTCAACACCGGGTCAACTTCTCTCTACTGCTTTTAAAGCAAG 453
|||||

QY 871 CGGTTCCGACCATCGCAGCCCGCCAGCTCAAGGGCTTTCTTCAAGTGCAGAGCAACC 929
DB 454 CGCTTTCGAGGATGGCGGGCGGTGCTCAAGGCTTTTTCGGCTGCAGAAACAGCC 512
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Search completed: February 12, 2005, 13:28:37
Job time : 3517 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 08:28:56 ; Search time 627 Seconds
(without alignments)
10564.897 Million cell updates/sec

Title: US-10-689-832-19
Perfect score: 1119
Sequence: 1 atggagcacgcacgcacca.....ctgtgtcatcatcctgtga 1119

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
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12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1119	100.0	1119	4 AAS15730	Aas15730 DNA encod
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3	1119	100.0	1119	12 ADI79322	Adi79322 NOV10a co
4	1119	100.0	1119	12 ADO56001	Ado56001 DNA encod
5	1119	100.0	1130	6 AAD29672	Aad29672 Human G-p
6	1119	100.0	2198	9 ACF05275	Acf05275 Human G-p
7	1091	97.5	1110	9 ACF05276	Acf05276 Human G-p
8	1091	97.5	2189	10 ADD18120	Add18120 Human G-p
9	1050	93.8	1059	6 ABN84269	Abn84269 Human che
10	1050	93.8	1062	6 ABK15562	Abk15562 cDNA enco
11	1050	93.8	1062	10 ACC71785	Acc71785 Human G p
12	1050	93.8	1202	8 ABV73364	Abv73364 Human TGR
13	1048.4	93.7	1062	6 ABK15563	Abk15563 cDNA enco
14	1048.4	93.7	1062	6 ABT04873	Abt04873 Human G p
15	1048.4	93.7	1062	10 ACC44115	Acc44115 Human AXO
16	1048.4	93.7	1343	4 AAS15731	Aas15731 DNA encod
17	1048.4	93.7	1343	10 ADJ87768	Adj87768 G-coupled
18	1048.4	93.7	1343	12 ADI79324	Adi79324 NOV11 cod
19	1048.4	93.7	1343	12 ADO56003	Ado56003 DNA encod
20	1048.4	93.7	1776	10 ADF70587	Adf70587 Orphan re

21	1048.4	93.7	2117	13 ADR16433	Adr16433 Human KOR
22	1048.4	93.7	2273	12 ADO28955	Ado28955 Human nov
23	1040.4	93.0	1526	6 AAD46858	Aad46858 Human 7TM
24	1040.4	93.0	1526	8 ACA60889	Aca60889 Human CDN
25	1040.4	93.0	1526	10 ABS57024	Abes57024 cDNA enco
26	934.8	83.5	1062	6 ABN84273	Abn84273 Human che
27	929.8	83.1	957	12 ADI79347	Adi79347 NOV10b co
28	929.8	83.1	957	12 ADO56026	Ado56026 DNA encod
29	926	82.8	1002	6 AAD27501	Aad27501 Human G-p
30	926	82.8	1002	10 AAD61658	Aad61658 Human GPC
31	926	82.8	1158	6 ABZ42880	Abz42880 Human GPC
32	926	82.8	1167	13 ADO89945	Ado89945 Antagonis
33	924.8	82.6	1000	6 AAD28102	Aad28102 Human thy
34	922.4	82.4	1032	6 ABN84271	Abn84271 Human che
35	922.4	82.4	1070	6 ABN84270	Abn84270 Human che
36	922.4	82.4	1826	6 ABN84272	Abn84272 Human che
37	918.8	82.1	946	10 ADJ87879	Adj87879 G-coupled
38	844.2	75.4	864	4 AAS42811	Aas42811 Human G p
39	832	74.4	1038	8 ABV73373	Abv73373 Mouse TGR
40	832	74.4	1038	12 ADO28957	Ado28957 Mouse nov
41	830	74.2	867	6 AAS98134	Aas98134 Human DNA
42	830	74.2	894	6 AAS98143	Aas98143 Human DNA
43	811.2	72.5	963	10 ADC12695	Adc12695 Human GPC
44	756.4	67.6	795	6 AAS98071	Aas98071 Human DNA
45	756.4	67.6	795	8 ABZ42552	Abz42552 Human G p

ALIGNMENTS

RESULT 1
AAS15730
ID AAS15730 standard; cDNA; 1119 BP.

XX AAS15730;

XX 14-FEB-2002 (first entry)

XX DNA encoding chemokine receptor family related protein, NOV10.

XX NOV; cytostatic; psoriasis; nootropic; neuroprotectant;
XX cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia;
XX haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;
XX differentiation; proliferation; haematopoiesis; wound healing;
XX angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;
XX haemophilia; allergy; Pendred syndrome; skeletal dysplasia;
XX ischaemic injury; neuroepithelial disorder; hepatitis; heart failure;
XX chemokine receptor; chromosome 1; 88.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1119

FT FT /*tag= a

FT FT /product= "Chemokine receptor related protein, NOV10"

FT FT sig_peptide 1..141

FT FT /*tag= b

FT FT mat_peptide 142..1116

FT FT /*tag= c

FT FT /note= "Mature chemokine receptor related protein, NOV10"

XX WO200170978-A2.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-US009093..

XX 20-MAR-2000; 2000US-0190768P.

XX 20-MAR-2000; 2000US-0190835P.

XX 22-MAR-2000; 2000US-0190972P.

XX 22-MAR-2000; 2000US-0191199P.

XX 24-MAR-2000; 2000US-0191947P.

XX 28-MAR-2000; 2000US-0192657P.

PR 28-MAR-2000; 2000US-0192664P.
 PR 28-MAR-2000; 2000US-0192665P.
 PR 28-MAR-2000; 2000US-0192984P.
 PR 29-MAR-2000; 2000US-0192836P.
 PR 31-MAR-2000; 2000US-0193843P.
 XX
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;
 PI Vernhet CAM;
 XX
 DR WPI; 2001-639127/73.
 DR P-PSDB; AAU10067.
 XX
 XX Polypeptides and nucleic acids related to chloride channel, insulin-like
 PT growth factor family of proteins, useful for diagnosing and treating
 PT cancer, cystic fibrosis, acute pancreatitis and Alzheimer's disease.
 XX
 XX Claim 9; Page 42; 15ipp; English.
 XX
 CC The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX
 CC polypeptides are useful for treating pathology associated with NOVX
 CC polypeptide, determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX, identifying agents binding to
 CC NOVX and treatment of disorders associated with altered expression of
 CC members of chloride channel-associated proteins e.g. cystic fibrosis and
 CC congenital myotonia. NOVX proteins are useful in treatment of disorders
 CC including psoriasis, cancer, diabetes, metabolic disorders of pancreas,
 CC e.g. acute pancreatitis, abnormal growth and accumulation of mast cells
 CC in one or more organs (e.g. haemophilia, anaemia), Pendred syndrome,
 CC skeletal dysplasias, disorders characterised by altered cell shape,
 CC motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial
 CC disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the
 CC treatment of disorders of vascular smooth muscle cell differentiation,
 CC (e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are
 CC useful to screen for molecules which inhibit or enhance NOVX activity or
 CC function and are useful as targets for the identifying small molecules,
 CC that modulate or inhibit e.g. neurogenesis, proliferation, motility, cell
 CC differentiation, haematopoiesis, wound healing and angiogenesis. NOV
 CC sequences are also useful for: identifying a cell or tissue type in a
 CC biological sample; amplifying DNA sequences from very small biological
 CC samples e.g. hair or skin or body fluids and as primers and probes to
 CC identify and/or clone NOVX homologues. NOVX proteins are useful
 CC immunogens to generate antibodies to monitor protein levels and modulate
 CC NOVX activity. Cells comprising the nucleic acids are useful for
 CC producing transgenic animals, for studying the function and/or activity
 CC of NOVX protein and identifying and/or evaluating modulators of NOVX
 CC protein activity. This sequence encodes NOV10 (located on chromosome 1)
 CC related to the chemokine receptor family of proteins, one of 12 NOV
 CC polypeptides described in the method of the invention
 XX
 XX Sequence 1119 BP; 258 A; 353 C; 220 G; 288 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 1119; DB 4; Length 1119;
 Best Local Similarity 100.0%; Pred. No. 1.3e-306;
 Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGCACACGACGCCCACTCGCAGCAACAGCTCGCTCTTTGGTGGTCCCGGC 60
 DB 1 ATGGAGCACACGACGCCCACTCGCAGCAACAGCTCGCTCTTTGGTGGTCCCGGC 60
 QY 61 TCGGCTCGGGCTTGGTTCGTCGCTGCTACTACAGCCTCTTGTGTCCTCGGT 120
 DB 61 TCGGCTCGGGCTTGGTTCGTCGCTGCTACTACAGCCTCTTGTGTCCTCGGT 120
 QY 121 TTACACAGCAAAATATCTTGAAGTATCTTCCAGCTGCTGCTGCGAAGACAGAAAG 180
 DB 121 TTACACAGCAAAATATCTTGAAGTATCTTCCAGCTGCTGCTGCGAAGACAGAAAG 180
 QY 181 TCTCTCTCAACATATCTTGGACATCTGCTGCTGCGAATCTTGGTCTCTTTTCATA 240
 DB 181 TCTCTCTCAACATATCTTGGACATCTGCTGCTGCGAATCTTGGTCTCTTTTCATA 240

QY 241 GTGTTTGTGAGTCTTCTGTTGAAAGATTTCACTTTGAACATGACAGATGCTCAGGTCCCC 300
 DB 241 GTGTTTGTGAGTCTTCTGTTGAAAGATTTCACTTTGAACATGACAGATGCTCAGGTCCCC 300
 QY 301 GACAAGATCATAGAAGTGTCTGGAATTTCTATCCATFCCAACCTCCATATGATGATCTGTA 360
 DB 301 GACAAGATCATAGAAGTGTCTGGAATTTCTATCCATFCCAACCTCCATATGATGATCTGTA 360
 QY 361 CCGTTAACCATTTGACAGGTATATCGTGTCTGACCCCGCTCAAGTACCAACCGTCTCA 420
 DB 361 CCGTTAACCATTTGACAGGTATATCGTGTCTGACCCCGCTCAAGTACCAACCGTCTCA 420
 QY 421 TACCCAGCCCGCACCCGGAAGTCAATGTAAGTGTTTACATCACCTGCTTCTCTGACCAAGC 480
 DB 421 TACCCAGCCCGCACCCGGAAGTCAATGTAAGTGTTTACATCACCTGCTTCTCTGACCAAGC 480
 QY 481 ATCCCTTATTAATCTGTTGGCCCAACATCTGGAATGGAAGTACATCAGCACTCTGTGTGAT 540
 DB 481 ATCCCTTATTAATCTGTTGGCCCAACATCTGGAATGGAAGTACATCAGCACTCTGTGTGAT 540
 QY 541 CAGTCTCTCATCTGGATCCATCTGTTACCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 541 CAGTCTCTCATCTGGATCCATCTGTTACCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 601 ATCTTGAACCTCAATCATTTGTGTACAAAGCTCAGGAGGAGAGCAATTTTCTGCTCCGTGGC 660
 DB 601 ATCTTGAACCTCAATCATTTGTGTACAAAGCTCAGGAGGAGAGCAATTTTCTGCTCCGTGGC 660
 QY 661 TACTCCACGGGGAAGACACCGCCATCTTGTTCACCAATTAATCTCACTTTTGGCCACATTT 720
 DB 661 TACTCCACGGGGAAGACACCGCCATCTTGTTCACCAATTAATCTCACTTTTGGCCACATTT 720
 QY 721 TGGGCCCCCCCCCATCATCATCATGATTTTACCACTTATGCGGGGGCCCATCCAGAACCGC 780
 DB 721 TGGGCCCCCCCCCATCATCATCATGATTTTACCACTTATGCGGGGGCCCATCCAGAACCGC 780
 QY 781 TGGCTGTGTACATCATCTGCGACATTTGCCCAACATGCTAGCCCTTCTGAAACACAGCCATC 840
 DB 781 TGGCTGTGTACATCATCTGCGACATTTGCCCAACATGCTAGCCCTTCTGAAACACAGCCATC 840
 QY 841 AACTTTCTTCTCTACTGTCTTTCATCAGCAAGCGGTTTCCGACCATGCGCAGCGCCACGCTC 900
 DB 841 AACTTTCTTCTCTACTGTCTTTCATCAGCAAGCGGTTTCCGACCATGCGCAGCGCCACGCTC 900
 QY 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTACACCAATCAATCACTTTTCC 960
 DB 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTACACCAATCAATCACTTTTCC 960
 QY 961 ATAAACAGTAGCCCTCGATCTCGCCGCAAACTCACACTGCTCAAGATGCTGTGTATAC 1020
 DB 961 ATAAACAGTAGCCCTCGATCTCGCCGCAAACTCACACTGCTCAAGATGCTGTGTATAC 1020
 QY 1021 CAGTATGACAAAAATGGAACCTTATAAAAAAGTGTATATGACAGCAAAAGCTCTCTACAG 1080
 DB 1021 CAGTATGACAAAAATGGAACCTTATAAAAAAGTGTATATGACAGCAAAAGCTCTCTACAG 1080
 QY 1081 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 1119
 DB 1081 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 1119
 RESULT 2
 ADJ87766
 ID ADJ87766 standard; DNA; 1119 BP.
 XX
 AC ADJ87766;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE G-coupled protein receptor-related protein coding sequence #56.
 XX novel protein; G-coupled protein receptor-related protein;
 KW cardiomyopathy; atherosclerosis; cell signal processing-related disorder;

KW Ophthalmological; Antipsoriatic; Neuroprotective; Nootropic;
 KW Antiarteriosclerotic; Hypotensive; Cardiant; Cerebroprotective;
 KW Gene Therapy; NOVX; human; cancer; myelogenous leukaemia;
 KW congenital neonatal autoimmune thrombocytopaenia; immunological disorder;
 KW allergy; infection; asthma; lung disease; reproductive disorder;
 KW haemangioma; deafness; liver cirrhosis; hepatitis C; gastric disorder;
 KW diabetic retinopathy; psoriasis; multiple sclerosis; atherosclerosis;
 KW hypertension; stroke; heart failure; chromosome 1; NOV10a;
 KW chemokine receptor; gene; db.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1119
 FT /tag= a
 FT /product= "NOV10a"
 XX
 PN WO2004009635-A2.
 XX
 XX 29-JAN-2004.
 XX
 XX 04-OCT-2001; 2001WO-US031292.
 XX
 XX 20-MAR-2001; 2001US-00813432.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;
 PI Vernet CAM;
 PI
 XX WPI; 2004-123380/12.
 DR P-PSDB; ADI79323.
 DR
 XX
 PS Claim 8; Page 41; 158pp; English.
 XX
 CC The present invention relates to novel NOVX proteins and their coding
 CC sequences (ADI79304-ADI79327). The sequences are useful for the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease associated with the NOVX protein, or for diagnosing and treating
 CC disorders associated with the NOVX protein, such as cancer, myelogenous
 CC leukaemia, congenital neonatal autoimmune thrombocytopaenia,
 CC immunological disorders, allergy and infection, asthma, lung diseases,
 CC reproductive disorders, male and female reproductive diseases,
 CC haemangioma, deafness, liver cirrhosis, hepatitis C, gastric disorders,
 CC diabetic retinopathy, psoriasis, multiple sclerosis, atherosclerosis,
 CC hypertension, stroke and heart failure. NOV10a represents a new member of
 CC the chemokine receptor family and the gene is located on chromosome 1.
 XX
 SQ Sequence 1119 BP; 258 A; 353 C; 220 G; 288 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1119; DB 12; Length 1119;
 Best Local Similarity 100.0%; Pred. No. 1.3e-306;
 Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGCACACGACGACCCACCTCGCAGCACACGCTCGTGTCTTGGTGTCCTCGGT 60
 Db 1 ATGGAGCACACGACGACCCACCTCGCAGCACACGCTCGTGTCTTGGTGTCCTCGGT 60
 QY 61 TCGGCTCGGGCTTGGGTTTCGTGCGCGTGTCTACTACAGCCTCTTGTGTGCTCGGT 120
 Db 61 TCGGCTCGGGCTTGGGTTTCGTGCGCGTGTCTACTACAGCCTCTTGTGTGCTCGGT 120
 QY 121 TTACAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAG 180
 Db 121 TTACAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAG 180
 QY 181 TCCTCCTACAATCTCTTGGCACTCGCTGCTGCGGACATCTGTCTCTTTTCATA 240
 Db 181 TCCTCCTACAATCTCTTGGCACTCGCTGCTGCGGACATCTGTGCTCTTTTCATA 240
 QY 241 GTGTTGTGGACTTCTCTGTGGAAGATTTTCATCTTGAACATGCAGATGCCTCAGTCCCC 300
 Db 241 GTGTTGTGGACTTCTCTGTGGAAGATTTTCATCTTGAACATGCAGATGCCTCAGTCCCC 300

QY 301 GACAGATCATAGAGTCTGGATTCTCATCCATCCACACCTCCATATGGATTACTGTA 360
 Db 301 GACAGATCATAGAGTCTGGATTCTCATCCATCCACACCTCCATATGGATTACTGTA 360
 QY 361 CGGTTAAACCATTTGACAGGTATATCGTCTCTGCGACCCGCTCAAGTACACACGGTCTCA 420
 Db 361 CGGTTAAACCATTTGACAGGTATATCGTCTCTGCGACCCGCTCAAGTACACACGGTCTCA 420
 QY 421 TACCCAGCCCGACCCCGAAAGTCAATTGTAAGTGTTTATCATCATCTGTTCTCTGACGAC 480
 Db 421 TACCCAGCCCGACCCCGAAAGTCAATTGTAAGTGTTTATCATCATCTGTTCTCTGACGAC 480
 QY 481 ATCCCTTATTACTGGTGGCCCAACATCTGGAGTGAAGACTACATCAGCACCTCTGTGAT 540
 Db 481 ATCCCTTATTACTGGTGGCCCAACATCTGGAGTGAAGACTACATCAGCACCTCTGTGAT 540
 QY 541 CACGTCCTCATCTGGATCCACTGTCTTACCCTGTACCTGTGGTGGCCCTGCTCCATCTTCTTC 600
 Db 541 CACGTCCTCATCTGGATCCACTGTCTTACCCTGTACCTGTGGTGGCCCTGCTCCATCTTCTTC 600
 QY 601 ATCTTGAACCTCAATCATTTGTGTACAAGCTCAGGAGGAAGACAAATTTTCGTCTCCGTGGC 660
 Db 601 ATCTTGAACCTCAATCATTTGTGTACAAGCTCAGGAGGAAGACAAATTTTCGTCTCCGTGGC 660
 QY 661 TACTCCACGGGAGAGACCCGCCATCTTGTTCACCATTTACTCCATCTTTGCCACACTT 720
 Db 661 TACTCCACGGGAGAGACCCGCCATCTTGTTCACCATTTACTCCATCTTTGCCACACTT 720
 QY 721 TGGGCCCCCGCATCATCATGATTTCTTACCACCTCTATGGGGGCCCATCCAGAACCGC 780
 Db 721 TGGGCCCCCGCATCATCATGATTTCTTACCACCTCTATGGGGGCCCATCCAGAACCGC 780
 QY 781 TGGCTGTGTACATCATATGTCGACATTTGCCAATGTCCAACTGTAGCCCTTCTGAAACACAGCCATC 840
 Db 781 TGGCTGTGTACATCATATGTCGACATTTGCCAATGTCCAACTGTAGCCCTTCTGAAACACAGCCATC 840
 QY 841 AACTTCTTCTTCTACTGTCTTATCAGCAAGCGGTTCCGACATCGGAGCGCGCCAGCTC 900
 Db 841 AACTTCTTCTTCTACTGTCTTATCAGCAAGCGGTTCCGACATCGGAGCGCGCCAGCTC 900
 QY 901 AAGCTTCTTCTTCAAGTGCAGAACCACTGTACAGTTCTACACCAATCATAACTTTTTC 960
 Db 901 AAGCTTCTTCTTCAAGTGCAGAACCACTGTACAGTTCTACACCAATCATAACTTTTTC 960
 QY 961 ATAAAGTATAGCCCTTGGATCTCGCGGCAAACTCACATCGCATCAAGATGCTGGTGTAC 1020
 Db 961 ATAAAGTATAGCCCTTGGATCTCGCGGCAAACTCACATCGCATCAAGATGCTGGTGTAC 1020
 QY 1021 CAGTATGCAAAAATGGAAAACCTTATAAAAAGTGTATGACAGCAAAAGCTCCTTACCAG 1080
 Db 1021 CAGTATGCAAAAATGGAAAACCTTATAAAAAGTGTATGACAGCAAAAGCTCCTTACCAG 1080
 QY 1081 TTTGGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 1119
 Db 1081 TTTGGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 1119
 RESULT 4
 ID ADO56001 standard; cDNA; 1119 BP.
 XX
 AC ADO56001;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 XX DNA encoding human NOV10.
 XX human; gene; ss; cancer; obesity; diabetic nephropathy;
 KW acute pancreatitis; stroke; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX

PN US2004058862-A1.
XX 25-MAR-2004.
XX 18-SEP-2002; 2002US-00246583.
XX 18-SEP-2002; 2002US-00246583.
XX (MAJU//) MAJUMDER K.
XX Majumder K;
XX WPI; 2004-268835/25.
XX P-PSDB; ADO56002.
XX Novel NOVX polypeptides, useful for treating cancer, obesity, diabetic
XX nephropathy, acute pancreatitis, strokes and multiple sclerosis.
XX Claim 9; Page 26-27; 87pp; English.
XX The invention relates to novel isolated NOVX nucleic acids and encoded
XX polypeptides. The nucleic acids, polypeptides and antibodies raised
XX against the polypeptides are useful for preventing or treating diseases
XX associated with aberrant NOVX expression or activity e.g., cancer,
XX obesity, diabetic nephropathy, acute pancreatitis, stroke, multiple
XX sclerosis. The present sequence represents a NOVX nucleic acid of the
XX invention.
XX SQ Sequence 1119 BP; 258 A; 353 C; 220 G; 288 T; 0 U; 0 Other;
Query Match 100.0%; Score 1119; DB 12; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.3e-306;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGCACAGCGCCACCTCGCAGCCAAACAGCTCGCTGCTTGGTGGTCCCGCG 60
DB 1 ATGGAGCACAGCGCCACCTCGCAGCCAAACAGCTCGCTGCTTGGTGGTCCCGCG 60
QY 61 TCGGCTCGGGCTTGGGTTTGGTGGCGGCTTACTACAGCCCTTGTGTCCTCGGT 120
DB 61 TCGGCTCGGGCTTGGGTTTGGTGGCGGCTTACTACAGCCCTTGTGTCCTCGGT 120
QY 121 TTACAGCAAAATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAAG 180
DB 121 TTACAGCAAAATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAAG 180
QY 181 TCCTCTACAACTATCTCTTGGCAGTGGCTGCGGCAATCTTGTCTCTTTTCATA 240
DB 181 TCCTCTACAACTATCTCTTGGCAGTGGCTGCGGCAATCTTGTCTCTTTTCATA 240
QY 241 GTGTTTGTGACTTCTCTTGGGAAGATTTTCATCTGAAATGAGATGCTCAGGTCC 300
DB 241 GTGTTTGTGACTTCTCTTGGGAAGATTTTCATCTGAAATGAGATGCTCAGGTCC 300
QY 301 GACAGATCATAGAGTGTGGAATTCATCATCAACCTCCATATGATGATTA 360
DB 301 GACAGATCATAGAGTGTGGAATTCATCATCAACCTCCATATGATGATTA 360
QY 361 CGGTTAACCAATTCACAGGTATATCGCTGCTGCGCCAGCTCAACCAAGCTCA 420
DB 361 CGGTTAACCAATTCACAGGTATATCGCTGCTGCGCCAGCTCAACCAAGCTCA 420
QY 421 TACCCAGCCCGCACCCGGAAGTCATTTGAAGTGTGTTTACATCACTGCTTCTGACCAG 480
DB 421 TACCCAGCCCGCACCCGGAAGTCATTTGAAGTGTGTTTACATCACTGCTTCTGACCAG 480
QY 481 ATCCCTTATTAATGTTGGGCCCAACATCTGAGCTGAAGACTACATGAGCACTTGTGCAT 540
DB 481 ATCCCTTATTAATGTTGGGCCCAACATCTGAGCTGAAGACTACATGAGCACTTGTGCAT 540
QY 541 CAGGTCTCATCTGGATCACTGCTTTCACCGTCTACCTGGTGGCTGCTCCATCTTCTTC 600
DB 541 CAGGTCTCATCTGGATCACTGCTTTCACCGTCTACCTGGTGGCTGCTCCATCTTCTTC 600

QY 601 ATCTTGAACCTCAATCTTGTGTACAGCTCAGGAGGAAGAGCAATTTTCTCTCCGTGC 660
DB 601 ATCTTGAACCTCAATCTTGTGTACAGCTCAGGAGGAAGAGCAATTTTCTCTCCGTGC 660
QY 661 TACTCCACGGGGAAGACACCGCCATCTTGTTCACCATTTACCTCCATCTTTGCCACATT 720
DB 661 TACTCCACGGGGAAGACACCGCCATCTTGTTCACCATTTACCTCCATCTTTGCCACATT 720
QY 721 TGGGCCCCCGCATCATCATGATTTTACCACTCTATGGGGCGCCCATCCAGAACC 780
DB 721 TGGGCCCCCGCATCATCATGATTTTACCACTCTATGGGGCGCCCATCCAGAACC 780
QY 781 TGGCTGGTACACATCATGTCGACATTTGCCAATGCTAGCCCTTCTGAACACAGCCATC 840
DB 781 TGGCTGGTACACATCATGTCGACATTTGCCAATGCTAGCCCTTCTGAACACAGCCATC 840
QY 841 AACTTCTTCTCTACTGCTTTCATCAGCAAGCGGTTCCGCAACCATGGCAGCGCCAGCTC 900
DB 841 AACTTCTTCTCTACTGCTTTCATCAGCAAGCGGTTCCGCAACCATGGCAGCGCCAGCTC 900
QY 901 AAGGCTTCTTCAAGTCCAGAGCAACTGTACAGTTCTACACCAATCATTAATTTTCC 960
DB 901 AAGGCTTCTTCAAGTCCAGAGCAACTGTACAGTTCTACACCAATCATTAATTTTCC 960
QY 961 ATAACAAGTAGCCCTTGGATCTCGCGGCAAACTCACTGCATCAAGATGCTGTGTATC 1020
DB 961 ATAACAAGTAGCCCTTGGATCTCGCGGCAAACTCACTGCATCAAGATGCTGTGTATC 1020
QY 1021 CAGTATGACAAAATGGAAAACCTATATAAAGTGTATATGACAGCAAAAGCTCTTACCAG 1080
DB 1021 CAGTATGACAAAATGGAAAACCTATATAAAGTGTATATGACAGCAAAAGCTCTTACCAG 1080
QY 1081 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 1119
DB 1081 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 1119
RESULT 5
AAD29672
ID AAD29672 standard; cDNA; 1130 BP.
XX
AC AAD29672;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human G-protein coupled receptor (GCRC-6) cDNA.
XX
KW Human; G-protein coupled receptor; GCRC-6; cell proliferative disorder;
KW neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;
KW metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease; hypertension;
KW atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic;
KW osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW anemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening;
KW transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant;
KW nootropic; neuroprotective; cardiac; immunosuppressive; anorectic;
KW viricide; gene; BS.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12..1130
FT /tag= a
FT /product= "Human GCRC-6"
FT sig_peptide 12..152
FT /tag= b
FT mat_peptide 153..1127
FT /tag= c
FT /product= "Human mature GCRC-6"
XX
PN WO200210387-A2.
XX

PD 07-FEB-2002.
 XX 25-JUL-2001; 2001WO-US023433.
 XX 27-JUL-2000; 2000US-0221478P.
 PR 03-AUG-2000; 2000US-0223268P.
 PR 21-AUG-2000; 2000US-0227054P.
 PR 08-SEP-2000; 2000US-0231121P.
 PR 13-SEP-2000; 2000US-0232243P.
 PR 15-SEP-2000; 2000US-0232691P.
 PR 22-SEP-2000; 2000US-0235146P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
 PI Elliot VS, Runkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA;
 PI Yao MG, Lu Y, Tribouley CN, Policky JL, Kearney L, Gaul RC;
 PI Warren BA, Lee EA, Ding L;
 XX WPI: 2002-188744/24.
 DR P-PSDB; AAE18645.
 DR
 XX New human G-protein coupled receptor polypeptide for diagnosis,
 PT prevention and treatment of cell proliferative, neurological,
 PT cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
 PT disorders.
 XX
 XX Claim 5; Page 141; 150pp; English.
 XX
 CC The invention relates to novel human G-protein coupled receptors (GPEC)
 CC and their encoding polynucleotides. GPEC is useful as an immunogen for
 CC preparing monoclonal and polyclonal antibodies. GPEC is useful for
 CC diagnosing, treating and preventing a cell proliferative disorder (e.g.,
 CC hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy,
 CC Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's
 CC disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension,
 CC myocardial infarction), gastrointestinal disorder (e.g., gastritis,
 CC cirrhosis, Crohn's disease), an autoimmune/inflammatory disorder (e.g.,
 CC acquired immunodeficiency syndrome (AIDS), allergy, anemia, asthma,
 CC rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity,
 CC osteoporosis), and viral infections. GPEC is useful in a number of drug
 CC screening techniques, and to analyse the proteome of a tissue or cell
 CC type. GPEC is useful for creating knockin humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene
 CC therapy, to generate a transcript image of a tissue or cell type, for
 CC detecting differences in the chromosomal location due to translocation,
 CC inversion, etc., among normal, carrier or affected individuals, and as
 CC hybridization probes for mapping naturally occurring genomic sequences.
 CC GPEC is useful in Southern or northern analysis, dot blot or other
 CC membrane-based technologies, in PCR technologies, in dipstick, pin,
 CC multifomat enzyme linked immunosorbant (ELISA)-like assays, and in
 CC microarrays utilising fluids or tissues from patients to detect altered
 CC GPEC expression. The present sequence is human GPEC-6 cDNA
 XX
 SQ Sequence 1130 BP; 258 A; 357 C; 226 G; 289 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1119; DB 6; Length 1130;
 Best Local Similarity 100.0%; Pred. No. 1.3e-306;
 Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGCACAGCAGCCACCTCGCAGCAACAGCTCGCTCTTGGTGGTCCCGCGC 60
 DB 1119
 QY 61 TCGGCTCGCGCTTGGGTTTCGTGGCCGTGGTCTACTACAGCCTCTTGTGTGCTCGGT 120
 DB 72 TCGGCTCGCGCTTGGGTTTCGTGGCCGTGGTCTACTACAGCCTCTTGTGTGCTCGGT 131
 QY 121 TTACAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGAGACAGAG 180
 DB 132 TTACAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGAGACAGAG 191
 QY 181 TCCTCTACAACTATCTCTTGGCACTCGTGTGGCGACATCTTGTCTCTTTTCATA 240

DB 192 TCCTCTACAACTATCTCTTGGCACTCGTGTGGCGACATCTTGGTCTCTTTTCATA 251
 QY 241 GTGTTTGTGGACTTCTCTGTGGAGATTTCACTTTGAAATGCAATGCAAGTCCCTCAGGTCCCC 300
 DB 252 GTGTTTGTGGACTTCTCTGTGGAGATTTCACTTTGAAATGCAATGCAAGTCCCTCAGGTCCCC 311
 QY 301 GACAGATCATAGAGTGTGGATTTCTCATCCATCCACACCTCCATATGGATTAATCTGTA 360
 DB 312 GACAAGATCATAGAGTGTGGATTTCTCATCCATCCACACCTCCATATGGATTAATCTGTA 371
 QY 361 CGGTTAACTTGCAGAGTGTATCGTGTCTGGCCACCGCTCAAGTACACACGCTCTCA 420
 DB 372 CGGTTAACTTGCAGAGTGTATCGTGTCTGGCCACCGCTCAAGTACACACGCTCTCA 431
 QY 421 TACCAGCCCGCACCCGAAAGTCAATTAAGTGTATACATCACTGTCTCTGACACGAGC 480
 DB 432 TACCAGCCCGCACCCGAAAGTCAATTAAGTGTATACATCACTGTCTCTGACACGAGC 491
 QY 481 ATCCCTTATTACTGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 540
 DB 492 ATCCCTTATTACTGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 551
 QY 541 CAGGTCTCTCATCTGGATCCACTGTCTTACCGCTTACCTGTGGTGGCTGTCTCTCTTC 600
 DB 552 CAGGTCTCTCATCTGGATCCACTGTCTTACCGCTTACCTGTGGTGGCTGTCTCTCTTC 611
 QY 601 ATCTTGAATCAATCATCTGTGTACAAGCTCAGGAGGAAGAGCAATTTTGTCTCGTGGC 660
 DB 612 ATCTTGAATCAATCATCTGTGTACAAGCTCAGGAGGAAGAGCAATTTTGTCTCGTGGC 671
 QY 661 TACTCCAGGGGAGACACCGCCATCTTGTTCACCATTAATCTTGTGCGCACACTT 720
 DB 672 TACTCCAGGGGAGACACCGCCATCTTGTTCACCATTAATCTTGTGCGCACACTT 731
 QY 721 TGGGCCCCCGCGCATCATCATGATCTTTACACCTCTATGGGGGCCCATCCAGAAACGCG 780
 DB 732 TGGGCCCCCGCGCATCATCATGATCTTTTACACCTCTATGGGGGCCCATCCAGAAACGCG 791
 QY 781 TGGTGTGTACATCATCTCCGACANTGCCAACATGTAGGCCCTTCTGAAACACAGCCATC 840
 DB 792 TGGTGTGTACATCATCTCCGACANTGCCAACATGTAGGCCCTTCTGAAACACAGCCATC 851
 QY 841 AACTTCTTCTCTACTGTCTTATCAGCAAGCGGTTCCGACCATGCGCAGCGCCACGCTC 900
 DB 852 AACTTCTTCTCTACTGTCTTATCAGCAAGCGGTTCCGACCATGCGCAGCGCCACGCTC 911
 QY 901 AAGGCTTTCTTCAAGTGCAGAACCACTGTACAGTTCTTACACCAATCATAACTTTTCC 960
 DB 912 AAGGCTTTCTTCAAGTGCAGAACCACTGTACAGTTCTTACACCAATCATAACTTTTCC 971
 QY 961 ATAAAGTGTAGCCCTGGATCTCGCCGCAAACTACACTGCATCAAGATGTGTGTGTAC 1020
 DB 972 ATAAAGTGTAGCCCTGGATCTCGCCGCAAACTACACTGCATCAAGATGTGTGTGTAC 1031
 QY 1021 CAGTATGCAAAATGGAACCTATATAAAGTGTGTATGACAGCAAAAGCTCTTACCAG 1080
 DB 1032 CAGTATGCAAAATGGAACCTATATAAAGTGTGTATGACAGCAAAAGCTCTTACCAG 1091
 QY 1081 TTTGAAGATGCCATTTGGAGCTTGTGTCTATCATCTCTGTGA 1119
 DB 1092 TTTGAAGATGCCATTTGGAGCTTGTGTCTATCATCTCTGTGA 1130
 RESULT 6
 ID ACF05275
 XX ACF05275 standard; cDNA; 2198 BP.
 AC ACF05275;
 XX 06-NOV-2003 (first entry)
 XX Human G-protein coupled receptor HGPBMY34 cDNA.

XX HGRBM34; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;
KW human; neuroprotective; nootropic; tranquilizer; antimigraine;
KW neuroleptic; antianemic; antidepressant; anticonvulsant; antiparkinsonian;
KW cytoskeletal; cardiac; hypotensive; antiangiogenic; analgesic; anorectic;
KW anti-HIV; antiaesthetic; osteopathic; uropathic; antiulcer; antiallergic;
KW gene therapy; gene; ss.
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 1247..2165
XX /*tag= a
XX /product= "HGRBM34"
XX
XX WO2003050256-A2.
XX
XX 19-JUN-2003.
XX
XX 06-DEC-2002; 2002WO-US039290.
XX
XX 06-DEC-2001; 2001US-0338371P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Feder JN, Gopal S, Mintier GA, Ramanathan CS;
XX WPI; 2003-577295/54.
XX P-PSDB; ABR62521.
XX
XX New nucleic acid molecule encoding a human G-protein coupled receptor,
PT HGRBM34, useful for diagnosing, preventing or treating diseases
PT involving the receptor, for example Parkinson's disease, dementia,
PT asthma, hypertension or cancer.
XX
XX Claim 1; Fig 1A-B; 112pp; English.
XX
XX The present sequence is that of cDNA encoding human HGRBM34, a newly
CC identified G-protein coupled receptor (GPCR) belonging to the group of
CC 'Class A' GPCRs and showing homology to the Pfam model 7 transmembrane
CC receptor, rhodopsin family. The cDNA was isolated by screening expressed
CC sequence tag databases using GPCR sequences. HGRBM34, also referred to
CC as GPCR-P14 and/or GPCR-145, is highly expressed in brain (amygdala,
CC caudate nucleus, corpus callosum, hippocampus, thalamus, substantia
CC nigra), spinal cord and pituitary, indicating an association in
CC neurological systems and conditions. It is also expressed in the bone
CC marrow and testis. The invention provides HGRBM34 polynucleotides,
CC polypeptides and antibodies, expression vectors, host cells and antisense
CC molecules, methods for screening for modulators of HGRBM34 activity
CC and/or function, and methods for diagnosing, treating, preventing and
CC screening for disorders and diseases associated with abnormal HGRBM34
CC activity, including: a disorder related to aberrant G-protein coupled
CC signalling; a disorder related to aberrant cell cycle regulation;
CC neurological disorders; anxiety; headache; migraine; schizophrenia; manic
CC depression; delirium; dementia; severe mental retardation and
CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
CC syndrome; Parkinson's disease; brain disorders; spinal cord disorders;
CC affective disorders; neoplastic disorders; cardiovascular disorders;
CC acute heart failure; hypotension; hypertension; angina pectoris;
CC myocardial infarction; an immunological disorder; immune-related
CC disorders; endocrine diseases; growth disorders; neuropathic pain;
CC obesity; anorexia; HIV infections; cancers; bulimia; asthma; osteoporosis
CC ; psychosis; metabolic disorders; pituitary disorders; urinary retention;
CC ulcers; allergies; or benign prostatic hypertrophy (all claimed)
XX
XX Sequence 2198 BP; 456 A; 693 C; 581 G; 468 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1119; DB 9; Length 2198;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-306;
XX Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGAGACACGACGCCACCTCGCAGCAACAGCTCGCTGCTTGGTGGTCCCGCGC 60
|||||

1047 ATGAGACACACGACGCCACCTCGCAGCAACAGCTCGCTGCTTGGTGGTCCCGCGC 1106
QY
61 TCGGCTCGGGCTTGGGTTTCGTCGCCGCTGCTACTACAGCCCTCTTGTGCTCGCTCGGT 120
DB
1107 TCGGCTCGGGCTTGGGTTTCGTCGCCGCTGCTACTACAGCCCTCTTGTGCTCGCTCGGT 1166
QY
121 TTACACAGAAAATATCTTGAAGTATCTCTCCAGCTGGTGGCAAGAGAAGAAG 180
DB
1167 TTACACAGAAAATATCTTGAAGTATCTCTCCAGCTGGTGGCAAGAGAAGAAG 1226
QY
181 TCTCTCTACAACTATCTCTTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 240
DB
1227 TCTCTCTACAACTATCTCTTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 1286
QY
241 GTGTTTGTGGAATCTCTCTTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 300
DB
1287 GTGTTTGTGGAATCTCTCTTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 1346
QY
301 GACAGATCATAGAAAGTCTGGAATCTCTCATCATCAACACCTTCCATATGGAATTAATGTA 360
DB
1347 GACAGATCATAGAAAGTCTGGAATCTCTCATCATCAACACCTTCCATATGGAATTAATGTA 1406
QY
361 CGTTTAACCACTTGAAGTATCTCTGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 420
DB
1407 CGTTTAACCACTTGAAGTATCTCTGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 1466
QY
421 TACCCAGCCCGCACCGGAAAGTCTTGTGAAGTGTGTTACATCACCTGCTTCTTGACACGC 480
DB
1467 TACCCAGCCCGCACCGGAAAGTCTTGTGAAGTGTGTTACATCACCTGCTTCTTGACACGC 1526
QY
481 ATCCCTTATTTACTGTTGGGCCCAACATCTGGAAGTGAAGACTATACATGACGACCTTGTGCAAT 540
DB
1527 ATCCCTTATTTACTGTTGGGCCCAACATCTGGAAGTGAAGACTATACATGACGACCTTGTGCAAT 1586
QY
541 CAGCTCTCTCATCTGATTCACCTGCTTACCTGCTTACCTGCTGCTGCTGCTGCTGCTTCTTC 600
DB
1587 CAGCTCTCTCATCTGATTCACCTGCTTACCTGCTTACCTGCTGCTGCTGCTGCTGCTTCTTC 1646
QY
601 ATCTTGAAGTCAATCATCTGTTGACAGCTCAGAGGAGAGCAATTTTCTGCTTCTGCTGGC 660
DB
1647 ATCTTGAAGTCAATCATCTGTTGACAGCTCAGAGGAGAGCAATTTTCTGCTTCTGCTGGC 1706
QY
661 TACTCCAGGGGAGACACACCCCATCTTGTTCACCATTTACCTTCCATCTTTGCAACACTT 720
DB
1707 TACTCCAGGGGAGACACACCCCATCTTGTTCACCATTTACCTTCCATCTTTGCAACACTT 1766
QY
721 TGGGCCCCCGCATCATCATGATTTTACCACTCTATGCGGCGGCCCATTCAGAACCCG 780
DB
1767 TGGGCCCCCGCATCATCATGATTTTACCACTCTATGCGGCGGCCCATTCAGAACCCG 1826
QY
781 TGGGCTGGTACACATCATGTCGACATTTGCCAATGTCGACATTTCTGAAACACAGCCATC 840
DB
1827 TGGGCTGGTACACATCATGTCGACATTTGCCAATGTCGACATTTCTGAAACACAGCCATC 1886
QY
841 AACTTCTTCTCTCTACTGCTTCTATGACAGCGGTTTCCGACCATGAGCAGCCGCGCAGCTC 900
DB
1887 AACTTCTTCTCTCTACTGCTTCTATGACAGCGGTTTCCGACCATGAGCAGCCGCGCAGCTC 1946
QY
901 AAGGCTTTCTTCAAGTCCAGAGCAACCTGTGACAGTTCTACCAATCATTAATCTTTTTC 960
DB
1947 AAGGCTTTCTTCAAGTCCAGAGCAACCTGTGACAGTTCTACCAATCATTAATCTTTTTC 2006
QY
961 ATAAAGTGTAGCCCTTGGATCTCGCGGCAAACTCACCTGATCAAGATGCTGGGTGATC 1020
DB
2007 ATAAAGTGTAGCCCTTGGATCTCGCGGCAAACTCACCTGATCAAGATGCTGGGTGATC 2066
QY
1021 CAGTATGACAAAATGGAACCTTATAAAAGTCTGTAATGACAGCAAAAGCTCTTACCAG 1080
DB
2067 CAGTATGACAAAATGGAACCTTATAAAAGTCTGTAATGACAGCAAAAGCTCTTACCAG 2126
QY
1081 TTTGAAGATGCCATTTGGAGCTTGTGTCATCTCTCTGTA 1119
DB
2127 TTTGAAGATGCCATTTGGAGCTTGTGTCATCTCTCTGTA 2165

RESULT 7
ACF05276
ID ACF05276 standard; cDNA; 1110 BP.
XX AC ACF05276;
XX 06-NOV-2003 (first entry)
XX
DE Human G-protein coupled receptor HGPBMY34 variant cDNA.
XX
XX HGPBMY34; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;
KW human; neuroprotective; nootropic; tranquilizer; antimigraine;
KW neuroleptic; antianemic; antidepressant; anticonvulsant; antiparkinsonian;
KW cytostatic; cardiant; hypotensive; antianginal; analgesic; anorectic;
KW anti-HIV; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic;
KW gene therapy; Gene; ss.
XX
XX Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 1..1110
FT /*tag= a
FT /product= "HGPBMY34 variant"
XX
XX WO2003050256-A2.
XX
XX 19-JUN-2003.
XX
XX 06-DEC-2002; 2002WO-US039290.
XX
XX 06-DEC-2001; 2001US-0338371P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Feder JN, Gopal S, Mintier GA, Ramanathan CS;
XX
XX WPI: 2003-577295/54.
XX P-PSDB; ABR62522.
XX
XX New nucleic acid molecule encoding a human G-protein coupled receptor,
PT HGPBMY34, useful for diagnosing, preventing or treating diseases
PT involving the receptor, for example Parkinson's disease, dementia,
PT asthma, hypertension or cancer.
XX
XX Claim 1; Fig 2A-B; 112pp; English.
XX
XX The present sequence is that of cDNA encoding a variant of human
CC HGPBMY34 containing a deletion of 3 amino acids of the protein sequence
CC but expected to share at least some of the expression patterns and
CC function of HGPBMY34. This is a newly identified G-protein coupled
CC receptor (GPCR) belonging to the group of 'Class A' GPCRs and showing
CC homology to the Pfam model 7 transmembrane receptor, rhodopsin family.
CC HGPBMY34 (or GPCR-P14, GPCR-145) is highly expressed in brain (amygdala,
CC caudate nucleus, corpus callosum, hippocampus, thalamus, substantia
CC nigra), spinal cord and pituitary, indicating an association in
CC neurological systems and conditions. It is also expressed in the bone
CC marrow and testis. The invention provides HGPBMY34 polynucleotides,
CC polypeptides and antibodies, expression vectors, host cells and antisense
CC molecules, methods for screening for modulators of HGPBMY34 activity
CC and/or function, and methods for diagnosing, treating, preventing and
CC screening for disorders and diseases associated with abnormal HGPBMY34
CC activity, including: a disorder related to aberrant G-protein coupled
CC signaling; a disorder related to aberrant cell cycle regulation;
CC neurological disorders; anxiety; headache; migraine; schizophrenia; manic
CC depression; delirium; dementia; severe mental retardation and
CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
CC syndrome; Parkinson's disease; brain disorders; spinal cord disorders;
CC affective disorders; neoplastic disorders; cardiovascular disorders;
CC acute heart failure; hypotension; hypertension; angina pectoris;
CC myocardial infarction; an immunological disorder; immune-related
CC disorders; endocrinal diseases; growth disorders; neuropathic pain;

CC obesity; anorexia; HIV infections; cancers; bulimia; asthma; osteoporosis
CC ; psychosis; metabolic disorders; pituitary disorders; urinary retention;
CC ulcers; allergies; or benign prostatic hypertrophy (all claimed)
XX

SQ Sequence 1110 BP; 253 A; 351 C; 220 G; 286 T; 0 U; 0 Other;

Query Match 97.5%; Score 1091; DB 9; Length 1110;
Best Local Similarity 99.2%; Pred. No. 1.2e-298;
Matches 1110; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 ATGGAGCACAGCAGCCACCTCGACCCAAAGCTCGTGTCTGTGGTGTCTCCCGCCG 60

Db 1 ATGGAGCACAGCAGCCACCTCGACCCAAAGCTCGTGTCTGTGGTGTCTCCCGCCG 60

QY 61 TGGGCTCGGGCTTGGGTTTGGTGGTCTTACTACAGCCTTCTGTGCTCGCTCGGT 120

Db 61 TGGGCTCGGGCTTGGGTTTGGTGGTCTTACTACAGCCTTCTGTGCTCGCTCGGT 120

QY 121 TTACCAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAAG 180

Db 121 TTACCAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAAG 180

QY 181 TCCTCTACAACTATCTCTTGGCACTCGCTGTCGACATCTTGGTCTCTTTTTCATA 240

Db 181 TCCTCTACAACTATCTCTTGGCACTCGCTGTCGACATCTTGGTCTCTTTTTCATA 240

QY 241 GTGTTTGGGACTTCTCTTGGAGATTTTCATCTTGAACATGCAGATGCTCAGTCTCCC 300

Db 241 GTGTTTGGGACTTCTCTTGGAGATTTTCATCTTGAACATGCAGATGCTCAGTCTCCC 300

QY 301 GACAAAGATCATAGAAAGTCTGGAATTCATCTCCATCCACACCTCATATGATTAATCTGA 360

Db 301 GACAAAGATCATAGAAAGTCTGGAATTCATCTCCATCCACACCTCATATGATTAATCTGA 360

QY 361 CCGTTAACCAATTGACAGGTATATCGTGTCTGCCACCCGCTCAAGTACCAACAGTCTTCA 420

Db 361 CCGTTAACCAATTGACAGGTATATCGTGTCTGCCACCCGCTCAAGTACCAACAGTCTTCA 420

QY 421 TACCAGCCCGCACCCGGAAAGTCAATTGTAAGTGTTCATCACCTGCTTCTGACCAAGC 480

Db 421 TACCAGCCCGCACCCGGAAAGTCAATTGTAAGTGTTCATCACCTGCTTCTGACCAAGC 480

QY 481 ATCCCTATTACTGTGGGCCCAACAATCTGAGCTGAAGACTACATCAGCACCTCTGTGCAT 540

Db 481 ATCCCTATTACTGTGGGCCCAACAATCTGAGCTGAAGACTACATCAGCACCTCTGTGCAT 540

QY 541 CACGTCCTCATCTGGATCCACTGTTCACCGTCTACCTGTGGTGGCCCTGCTCCATCTTCTTC 600

Db 541 CACGTCCTCATCTGGATCCACTGTTCACCGTCTACCTGTGGTGGCCCTGCTCCATCTTCTTC 600

QY 601 ATCTTGAATCAATCATTTGTGTACAGCTCAGGAGGAGAGCAATTTTCGTCTCGTGGC 660

Db 601 ATCTTGAATCAATCATTTGTGTACAGCTCAGGAGGAGAGCAATTTTCGTCTCGTGGC 660

QY 661 TACTCCAGGGAGAGACCAACCGCATCTTGTTCACCATTTACTTCCATCTTTGCCACACTT 720

Db 661 TACTCCAGGGAGAGACCAACCGCATCTTGTTCACCATTTACTTCCATCTTTGCCACACTT 720

QY 721 TGGGCCCCCGCATCATCATGATTTCTTTTACACCTCTATGGGGGCCCATCCAGAACCGC 780

Db 721 TGGGCCCCCGCATCATCATGATTTCTTTTACACCTCTATGGGGGCCCATCCAGAACCGC 780

QY 781 TGGTGTGTACATCATGATCTCGACATTTGCCAATGCTAGCCCTTCTGAAACAGCCATC 840

Db 781 TGGTGTGTACATCATGATCTCGACATTTGCCAATGCTAGCCCTTCTGAAACAGCCATC 840

QY 841 AACTTCTTCTCTACTGTCTCATCAGCAAGCGTTTCCGACCATGGCAGCGCCACGCTC 900

Db 841 AACTTCTTCTCTACTGTCTCATCAGCAAGCGTTTCCGACCATGGCAGCGCCACGCTC 900

QY 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTTCTACACCAATCAATCTTTTCC 960

Db 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTTCTACACCAATCAATCTTTTCC 960

QY 901 AAGCGTTTCTCAAGTGCAGAGCAACCTGTACAGTTCTTACCAATCATTAATTTTCC 960
Db |||||||
QY 1947 AAGCGTTTCTCAAGTGCAGAGCAACCTGTACAGTTCTTACCAATCATTAATTTTCC 2006
Db |||||||
QY 961 ATAACAGTAGCCCTTGGATCTCGCGGCAAACTCACATGATCAAGATGCTGTGTAC 1020
Db |||||||
QY 2007 ATAACAGTAGCCCTTGGATCTCGCGGCAAACTCACATGATCAAGATGCTGTGTAC 2066
QY 1021 CAGTATGACAAAATGGAACCTATATAAAGTGTGTATGACAGCAAAAGCTCTTACCAG 1080
Db |||||||
QY 2067 CAGTATGACAAAATGGAACCTATATAAAGTGTGTATGACAGCAAAAGCTCTTACCAG 2117
QY 1081 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 1119
Db |||||||
QY 2118 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGA 2156

RESULT 9
ABN84269
ID ABN84269 standard; cDNA; 1059 BP.
XX AC ABN84269;
XX DT 23-SEP-2002 (first entry)
XX DE Human chemokine-like receptor cDNA.
XX KW Chemokine-like receptor; G-protein coupled receptor; receptor; human;
KW HIV infection; cardiovascular disease; asthma;
KW chronic obstructive pulmonary disease; cardiant; antiasthmatic;
KW vasotropic; hypotensive; antiarrhythmic; thrombolytic; anticoagulant;
KW antiinflammatory; antiallergic; immunomodulator; gene therapy; gene; ss.
XX OS Homo sapiens.

XX FH Location/Qualifiers
XX FT 1. .1059
XX FT /*tag= a
XX FT /partial
XX FT /product= "Chemokine-like receptor"
XX FT /note= "the CDS does not include a stop codon"
XX PN WO200248358-A2.
XX PD 20-JUN-2002.
XX PF 12-DEC-2001; 2001WO-BP014571.
XX PR 14-DEC-2000; 2000US-0255150P.
XX PR 02-APR-2001; 2001US-0280110P.
XX PR 21-JUN-2001; 2001US-0299474P.
XX PA (FARB) BAYER AG.
XX PI Smolyar A, Zhu Z, Encinas J, Watanabe S, Okigami H;
XX DR WPI; 2002-547858/58.
XX DR P-PSDB; AB579517.

XX New isolated polynucleotide encoding a chemokine-like receptor
PT polypeptide for treating e.g. asthma, myocardial infarction, human
PT immunodeficiency virus infection, or chronic obstructive pulmonary
PT disease.
XX Claim 1; Fig 1; 114pp; English.
XX The present sequence is that of cDNA encoding a novel human chemokine-
CC like receptor (see AN79517) of 353 amino acids and having 7 putative
CC transmembrane domains, consistent with the structure of a G-protein
CC coupled receptor. Its closest human homologue is C-C chemokine receptor
CC 3. The novel receptor is expressed at low levels in most tissues. It is
CC expressed at a high level in phytohaemagglutinin-stimulated CD8+ cells,
CC but in none of the other immune cells tested. It may act as a receptor of

CC chemoattractant molecules on activated lymphocytes and be involved in
CC cell trafficking and homing to sites of infection, inflammation or tissue
CC injury. Regulation of activity of the novel receptor can therefore be
CC used to treat cardiovascular, immunological and inflammatory diseases,
CC including asthma and chronic obstructive pulmonary disease (COPD). The
CC receptor may also be a target for viruses that reside in the nervous
CC system. Regulating the binding of ligands, e.g. chemoattractant molecules
CC or virus particles, to the receptor can therefore be used to modulate the
CC immune response to inhibit viral infections, including HIV infection. A
CC claimed method of reducing activity of the receptor involves contacting a
CC cell with a reagent (preferably an antibody, antisense oligonucleotide or
CC ribozyme) to a product (preferably RNA or a polypeptide) encoded by a
CC polynucleotide encoding the human chemokine-like receptor in vivo or in
CC vitro. A claimed method of treating a chemokine-like receptor dysfunction
CC related disease selected from HIV infection, a cardiovascular disorder,
CC asthma or COPD uses a reagent that modulates a function of the receptor
XX
SQ Sequence 1059 BP; 240 A; 342 C; 206 G; 271 T; 0 U; 0 Other;

Query Match 93.8%; Score 1050; DB 6; Length 1059;
Best Local Similarity 100.0%; Pred. No. 4.9e-287;
Matches 1050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGCACACGACGCGCCACCTCGCAGCCAAACAGCTCGCTGTCTTGGTGGTCCCCCGCG 60
Db |||||||
QY 61 TCGGCTCGCGCTTGGGTTTCGTGCCGTGTCTACTACAGCCTTTGCTGTGCTCGGT 120
Db |||||||
QY 121 TTACAGCAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAGAAG 180
Db |||||||
QY 181 TCCTCTCAACTATCTCTGGCACTGCTGCGACATCTTGGTCTCTTTTTCATA 240
Db |||||||
QY 241 GTGTTGTGGACTTCTGTGGAAAGATTTCATCTTGAACATGCAGATGCCTCAGGTCCC 300
Db |||||||
QY 301 GACAGATCATAGAAGTGTGGAATTTCTATCCATCCACACTCCATATGATGATCTGTA 360
Db |||||||
QY 361 CCGTTAACCATTTGACAGGTATATCGTGTCTGCCACCGCTCAAGTACACACGGTCTCA 420
Db |||||||
QY 421 TACCCAGCCCGCACCCCGGAAAGTTCATCTTGAAGTGTGTACATCACCTCTCTGACCA 480
Db |||||||
QY 481 ATCCCTATTTACTGTTGGTGGCCCAACATCTGGAGTGAAGACTACATCAGACCTCTGTG 540
Db |||||||
QY 541 CAGTCTCATCTGTGATCCACTGTTCACCGTCTTACCTGGTGGCCCTGCTCATCTTCTTC 600
Db |||||||
QY 601 ATCTTGAACCTCAATCTGTTGTACAGCTCAGGAGGAAGAGCAATTTTCGTCTCGTGGC 660
QY 661 TACTCCAGGGGAGACACCGCCATCTTGTTCACCATTAACCTCACTTTTGGCACACTT 720
Db |||||||
QY 721 TGGGCCCCCCCCCATCATCATGATTTTACCACCTCTATGGGGGGCCCATCCAGAACCGC 780
Db |||||||

Db 721 TGGGCCCCCGCATCATCATGATCTTTTACCACCTCTATGGGGCGCCCATCCAGAACCGC 780
Qy 781 TGCGTGGTACATCATGTCGACATTCGCAACATGCTAGCCCTCTTGAAACAGCCATC 840
Db 781 TGCGTGGTACATCATGTCGACATTCGCAACATGCTAGCCCTCTTGAAACAGCCATC 840
Qy 841 AACTTCTTCTCTACTGCTTCATCAGCAGCGGTTCCGACCACTGCTGACCACTGCGCCGCGCAGCTC 900
Db 841 AACTTCTTCTCTACTGCTTCATCAGCAGCGGTTCCGACCACTGCTGACCACTGCGCCGCGCAGCTC 900
Qy 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTTACACCAATCATAACTTTTCC 960
Db 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTTACACCAATCATAACTTTTCC 960
Qy 961 ATAACAAGTAGCCCTTGGATCTGCGCGCAAACTCACACTGATCAAGATGCTGGTGTAC 1020
Db 961 ATAACAAGTAGCCCTTGGATCTGCGCGCAAACTCACACTGATCAAGATGCTGGTGTAC 1020
Qy 1021 CAGTATGACAAAATGGAACCTATAAA 1050
Db 1021 CAGTATGACAAAATGGAACCTATAAA 1050

RESULT 10

ABK15562
ID ABK15562 standard; cDNA; 1062 BP.
XX
AC ABK15562;
DT
DT
XX 08-MAY-2002 (first entry)
DE cDNA encoding novel G-protein coupled receptor TGR8, version #1.
XX
KW G-protein coupled; receptor; cardiovascular; immunomodulator; TGR8;
KW cytosolic; antiinflammatory; antiulcer; fetal brain;
KW central nervous system disease; circulatory organ disorder; cancer;
KW metabolic disease; immunological disease; gastrointestinal disease;
KW gene therapy; transgenic animal; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..1062
FT CDS /*tag= a
FT /product= "TGR8"
FT /note= "G-protein coupled receptor"
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PN WO200194582-A1.
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PD 13-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-JP004643.
XX
PR 02-JUN-2000; 2000JP-00170446.
PR 23-JUN-2000; 2000JP-00194926.
XX (TAKE) TAKEDA CHEM IND LTD.
XX PA
XX PI Terao Y, Matsui H, Shintani Y;
XX
XX WPI; 2002-164317/21.
DR P-PSDB; AAU76416.
XX
PT Human fetal brain-originated G protein-coupled receptor protein TGR8 and
PT encoding DNA, for developing drugs to treat e.g. diseases of the central
PT nervous system or circulatory organs, cancer, and metabolic diseases.
XX
PS Claim 5; Page 94; 102pp; Japanese.
XX
CC The invention describes a human fetal brain-originated G protein-coupled
CC receptor protein, or its salt. The protein and encoded DNA are useful for
CC developing drugs to treat e.g. diseases of the central nervous system or
CC circulatory organs, cancer, metabolic diseases, immunological diseases

CC and gastrointestinal diseases. The invention also describes creation of a
CC probe for gene therapy and construction of a transgenic animal. This
CC sequence encodes the novel G-protein coupled receptor TGR8, described in
CC the method of the invention

SQ Sequence 1062 BP; 241 A; 342 C; 207 G; 272 T; 0 U; 0 Other;

Query Match 93.8%; Score 1050; DB 6; Length 1062;
Best Local Similarity 100.0%; Pred. No. 4.9e-287;
Matches 1050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 CCGTTAAACATGACAGTATATCGTCTGCGCACCCGCTCAAGTACCAACAGGTCTCA 420
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Db 721 TGGGCCCCCGCATCATCATGATCTTTTACACCTCTATGGGGCGCCCATCCAGAACCGC 780
Qy 781 TGGCTGGTACACATCATGTCGACATTCGCAACATGCTAGCCCTTCTGAACACAGCCATC 840
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Qy 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTTACCACTCAAGATGCTGGTGTAC 960
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KW	G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;
KW	antipneumonic; nontropic; neuroprotective; antianemic; antitumor; human;
KW	antiparkinsonian; antileukemic; TGR20; gene; ds.
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OS	Homo sapiens.
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FT	/product= "TGR20"
FT	/note= "GPCR polypeptide"
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DN	WO200277001-A2.
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PD	03-OCT-2002.
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PF	08-MAR-2002; 2002WO-US007171.
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PR	09-MAR-2001; 2001US-00802803.
PR	16-MAR-2001; 2001US-0276649P.
XX	
XX	(TULA-) TULARIK INC.
PA	
XX	
PI	Tian H, Zhao J, Chen J, Cutler G;
XX	
DR	WPI; 2003-018881/01.
DR	P-PSDB; ABB82499.
XX	
PT	New G-protein coupled receptor polypeptides and polynucleotides useful
PT	for identifying compounds for treating a TGR-associated disorder, e.g.
PT	psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's
PT	disease, anemia.
XX	
PS	Claim 6; Page 63; 87pp; English.
XX	
CC	The invention relates to G-protein coupled receptor (GPCR) polypeptides
CC	and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR183,
CC	TGR341, TGR211, and TGR79. The polypeptides and nucleic acids are
CC	useful for identifying compounds for treating a TGR-associated disorder,
CC	such as psoriasis, inflammatory bowel disease, hyperlipidemia,
CC	Parkinson's disease, Huntington's disease, anemia, immune and blood
CC	disorders, ulcerative colitis, Crohn's disease or spleen enlargement.
CC	They are also useful for identifying cells such as kidney, liver,
CC	hypothalamus, colon, adipose, or spleen cells, for forensics and
CC	paternity determination, diagnosing diseases and examining signal
CC	transduction. The present sequence represents a human TGR20 polypeptide
CC	encoding DNA
XX	
SQ	Sequence 1202 BP; 267 A; 380 C; 258 G; 297 T; 0 U; 0 Other;
	Query Match 93.8%; Score 1050; DB 8; Length 1202;
	Best Local Similarity 100.0%; Pred. No. 5.2e-287;
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Dd	128 TCGGCCTCGCGCTTGGGTTTCGTGCGCGGTGTCTACTACAGCCTCTTGCTGTGCTCGGT 187
Qy	121 TTACCAGCAAAATATCTTGACAGTAGTATCATCTCTCCAGCTGTGGGAAGAAGACAGAG 180
Dd	188 TTACCAGCAAAATATCTTGACAGTAGTATCATCTCTCCAGCTGTGGGAAGAAGACAGAG 247
Qy	181 TCCTTCCTACAACTATCTCTTGCGCACTCGCTGCTCGCGACATCTTGGTCTCTTTTTTCATA 240
Dd	248 TCCTTCCTACAACTATCTCTTGCGCACTCGCTGCTCGCGACATCTTGGTCTCTTTTTTCATA 307
Qy	241 GTGTTTGTGGACTTCCTGTTGGGAAGATTTCATCTTTGAACATGCAGATGCTCAGGTCCCC 300
Dd	308 GTGTTTGTGGACTTCCTGTTGGGAAGATTTCATCTTTGAACATGCAGATGCTCAGGTCCCC 367

XX (AREN-) ARENA PHARM INC.
 XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
 XX WPI; 2002-566565/60.
 XX P-PSDB; ABJ04075.
 XX Novel endogenous and non-endogenous versions of G protein-coupled
 PT receptor useful for identification of candidate compounds as receptor
 PT agonists or antagonists for use as therapeutic agents.
 XX Claim 31; Page 70; 84pp; English.
 XX The present invention provides the protein and coding sequences of
 CC several human G-protein coupled receptors (GPCRs). These can be used in
 CC the identification of candidate compounds as receptor agonists or inverse
 CC agonists having applicability as therapeutic agents. The present sequence
 CC is a GPCR coding sequence of the invention
 XX SQ Sequence 1062 BP; 240 A; 342 C; 208 G; 272 T; 0 U; 0 Other;
 Query Match 93.7%; Score 1048.4; DB 6; Length 1062;
 Best Local Similarity 99.9%; Pred. No. 1.4e-286;
 Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGGAGCACACGACGCCACCTCGCAGCAACAGAGCTCGCTGCTGTGGTGGTCCCGCGC 60
 DB 1 ATGGAGCACACGACGCCACCTCGCAGCAACAGAGCTCGCTGCTGTGGTGGTCCCGCGC 60
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 DB 421 TACCCAGCCCGCACCCGGAAGTCAATGTAAGTGGTTTATACACCTGCTTCTGACCAGC 480
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 ID ACC44115 standard; DNA; 1062 BP.
 XX ACC44115;
 XX 27-JUN-2003 (first entry)
 XX Human AXOR-57 coding sequence.
 DE ds; antibacterial; antifungal; antiviral; antiprotazoal; analgesic; gene;
 KW cytotatic; antidiabetic; anorectic; anabolic; antiaesthetic; antagonist;
 KW antiparkinsonian; cardiac; hypotensive; hypertensive; nephrotropic;
 KW osteopathic; antitropical; antitumor; antiallergic; antimigraine; agonist;
 KW antileptic; nootropic; tranquilizer; neuroprotective; antidepresant;
 KW vaccine; gene therapy; G-protein coupled receptor; receptor; infection;
 KW pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; stroke;
 KW Parkinson's disease; osteoporosis; angina pectoris; ulcer; allergy;
 KW vomiting; schizophrenia; depression; dementia; Huntington's disease.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 1..1062
 FT /*tag= a
 FT /product= "AXOR-57 protein"
 XX GB2365009-A.
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 XX 13-FEB-2002.
 PD
 XX 11-APR-2001; 2001GB-00009018.
 PP
 XX 11-APR-2001; 2001GB-00009018.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Elshourbagy N, Gattu M, Michalovich D, Shabon U;
 PI WPI; 2003-203569/20.
 DR P-PSDB; ABP98724.
 XX
 PT New G-protein coupled receptor, AXOR 57, for diagnosing and treating
 PT diseases, such as, pain, cancer, diabetes, obesity, anorexia, asthma,
 PT Parkinson's disease, hypotension, hypertension, urinary retention, and
 PT osteoporosis.

XX
PS Claim 2; Page 27; 32pp; English.

The invention relates to the isolation of the coding sequence of a novel G-protein coupled (7TM) receptor AXOR 95 (this sequence) or fragment encoding a polypeptide having at least 95% identity with AXOR-57 protein. The protein has been shown to have homology to the human chromosome 16 clone C17B-H1.036A2 (AC008785). The protein and polynucleotides encoding the protein are used in screening for compounds that stimulate or inhibit the function or level of the polypeptide or polynucleotides, such as, agonists and antagonists. The protein, polynucleotides, and antibodies to the protein are used in diagnostic kits, to diagnose a disease. Polynucleotides encoding the protein are used for chromosome localization studies, or for tissue expression studies. The protein and nucleic acids encoding the protein are used in vaccines for treating diseases such as, bacterial, fungal, protozoal, and viral infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcer, allergy, benign prostatic hypertrophy, migraine, vomiting, anxiety, schizophrenia, depression, delirium, dementia, severe mental retardation, or Huntington's disease

SQ Sequence 1062 BP; 240 A; 342 C; 208 G; 272 T; 0 U; 0 Other;

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Query Match          93.7%; Score 1048.4; DB 10; Length 1062;
Best Local Similarity 99.9%; Pred. No. 1.4e-286;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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12	1040.4	93.0	1062	6	AX664703 Sequence
13	1040.4	93.0	1526	6	AX664701 Sequence
14	934.8	83.5	1062	6	AX463235 Sequence
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ALIGNMENTS

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DEFINITION Sequence 19 from Patent WO0170978.
ACCESSION AX254975
VERSION AX254975.1 GI:16074503
KEYWORDS
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Taupier,R.J., Majumder,K., Spaderna,S.K., Smithson,G., Mezes,P.S. and Vernet,C.A.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0170978-A 19 27-SEP-2001;
Curagen Corporation (US)
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LOCUS Sequence 1 from Patent WO0248358.
DEFINITION AX463227
ACCESSION AX463227
VERSION AX463227.1 GI:21886199
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Smolyar,A., Zhu,Z., Encinas,J., Watanabe,S. and Okigami,H.
Regulation of human chemokine-like receptor
Patent: WO 0248358-A 1 20-JUN-2002;
Bayer Aktiengesellschaft (DE)
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Query Match 93.8%; Score 1050; DB 6; Length 1059;
Best Local Similarity 100.0%; Pred. No. 6.5e-252;
Matches 1050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
BD183203 BD183203 1062 bp DNA linear PAT 17-JUN-2003
LOCUS Novel G protein-coupled receptor and its DNA.
DEFINITION BD183203
ACCESSION BD183203
VERSION BD183203.1 GI:31875403
KEYWORDS JP 2002345481-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1062)
Terao,Y., Matsui,H. and Shintani,Y.
Novel G protein-coupled receptor and its DNA
Patent: JP 2002345481-A 3 03-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT
OS Homo sapiens (human)
PN JP 2002345481-A/3
PD 03-DEC-2002
PF 01-JUN-2001 JP 2001166688
PI YASUKO TERA0, HIDEKI MATSUI, YASUSHI SHINTANI
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PC C12N5/10,C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
G01N33/53,
PC G01N33/566,C12N15/00,C12N5/00
CC Novel G protein-coupled receptor and its DNA
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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Query Match 93.8%; Score 1050; DB 6; Length 1062;
Best Local Similarity 100.0%; Pred. No. 6.5e-252;
Matches 1050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Novel G protein-coupled receptor and its DNA. linear PAT 27-AUG-2002
DEFINITION Novel G protein-coupled receptor and its DNA.
ACCESSION BD103851
VERSION BD103851.1 GI:22649425
KEYWORDS WO 0194582-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1062)
AUTHORS Terao,Y., Matsui,H. and Shintani,Y.
TITLE Novel G protein-coupled receptor and its DNA
JOURNAL Patent: WO 0194582-A 3 13-DEC-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,YASUKO TERAO,HIDEKI MATSUI,YASUSHI
SHINTANI
COMMENT OS Homo sapiens (human)
PN WO 0194582-A/3
PD 13-DEC-2001
PF 01-JUN-2001 WO 2001JP004643
PR 02-JUN-2000 JP 00P 170446,23-JUN-2000 JP 00P 194926 PI
YASUKO TERAO,HIDEKI MATSUI,YASUSHI SHINTANI
PC C12N15/12,C12P21/02,C07K14/705,C07K16/28,A61K45/00,A61P25/00,
PC A61P29/00,
PC A61P3/00,A61P35/00,A61P37/00,A61P1/00,A61P1/00,G01N33/566, PC
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CC Novel G protein-coupled receptor and its DNA
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.5e-252;
Matches 1050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION cds.
ACCESSION AY635179
VERSION AY635179.1 GI:49413551
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1167)
AUTHORS Bonner,T.I., Nagle,J.W. and Kauffman,D.
TITLE Complete coding sequence of GPR139
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1167)
AUTHORS Bonner,T.I., Nagle,J.W. and Kauffman,D.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2004) Lab of Genetics, NIMH, Bldg 36, Rm 3D06, MSC4094, Bethesda, MD 20892-4094, USA
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LOCUS			
Novel G protein-coupled receptor and its DNA.			
DEFINITION			
BD183204			
ACCESSION			
BD183204.1 GI:31875404			
VERSION			
JP 2002345481-A/4			
KEYWORDS			
Homo sapiens (human)			
SOURCE			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS			
Terao,Y., Matsui,H. and Shintani,Y.			
TITLE			
Novel G protein-coupled receptor and its DNA			
JOURNAL			
Patent: JP 2002345481-A 4 03-DEC-2002;			
COMMENT			
TAKEDA CHEMICAL INDUSTRIES LTD			
OS Homo sapiens (human)			
PN JP 2002345481-A/4			
PD 03-DEC-2002			
PF 01-JUN-2001 JP 2001166688			
PI YASUKO TERAOKA,HIDEKI MATSUI,YASUSHI SHINTANI			
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C12N1/21,			
PC C12N5/10,C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC			
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CC Novel G protein-coupled receptor and its DNA			
FH Key Location/Qualifiers			

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		Matches 1049; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
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Db	1	ATGAGGACACGACGACCCACCTCGCAGCCACAGCTCGCTGCTGTGGTGGTCCCGCGC	60	
QY	61	TGGGCTTGGGCTTGGGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	120	
Db	61	TGGGCTTGGGCTTGGGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	120	
QY	121	TTACAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGTGGTGGTGGTGGTGGT	180	
Db	121	TTACAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGTGGTGGTGGTGGTGGT	180	
QY	181	TCCTCTACAACTATCTCTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA	240	
Db	181	TCCTCTACAACTATCTCTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA	240	
QY	241	GTGTTTGGGACTTCTCTGTGGAAATTTCACTTTGAACATGCAGATGCCTCAGGTCCCC	300	
Db	241	GTGTTTGGGACTTCTCTGTGGAAATTTCACTTTGAACATGCAGATGCCTCAGGTCCCC	300	
QY	301	GACAAAGATCATAGAAAGTCTGGAATTTCTATCCATCCACACTCCATATGGAATTAATGA	360	
Db	301	GACAAAGATCATAGAAAGTCTGGAATTTCTATCCATCCACACTCCATATGGAATTAATGA	360	
QY	361	CGTTTAAACCATTTGACAGGTATATCGCTGTGCGCAACCGCTCAAGTACACACGCTCTCA	420	
Db	361	CGTTTAAACCATTTGACAGGTATATCGCTGTGCGCAACCGCTCAAGTACACACGCTCTCA	420	
QY	421	TACCCAGCCCGACCCCGGAAAGTCAATTGTAAGTGTTTACATCACCTGCTCTGACACAGC	480	
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QY	481	ATCCCTTATTAATGTTGGTGGCCCAACATCTGGAATGGAAGACTACATCAGCACCTCTGTGCAT	540	
Db	481	ATCCCTTATTAATGTTGGTGGCCCAACATCTGGAATGGAAGACTACATCAGCACCTCTGTGCAT	540	
QY	541	CAGGTCTCATCTGGATCCATGCTTCAACCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCT	600	
Db	541	CAGGTCTCATCTGGATCCATGCTTCAACCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCT	600	
QY	601	ATCTTGAACCTCAATCTGTTGTAAGCTCAGGAGGAGAGCAATTTTCTGCTCCGTGGC	660	
Db	601	ATCTTGAACCTCAATCTGTTGTAAGCTCAGGAGGAGAGCAATTTTCTGCTCCGTGGC	660	
QY	661	TACTTCCAGGGGAGAGACACCGCCATCTTGTTCACCATTTCTTTCACCATTTTTCACCAT	720	
Db	661	TACTTCCAGGGGAGAGACACCGCCATCTTGTTCACCATTTCTTTCACCATTTTTCACCAT	720	
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Db	721	TGGGCCCCCGCATCATCATGATTTCTTTACCACTCTATGGGGCGCCCATCCAGAACCGC	780	
QY	781	TGGTGGTACACATCATGTCCGACATTTGCCAACTAGTCCCTTCTGAAACACAGCCATC	840	
Db	781	TGGTGGTACACATCATGTCCGACATTTGCCAACTAGTCCCTTCTGAAACACAGCCATC	840	
QY	841	AACTTCTTCTCTACTGCTTCTATGCAAGCGGTTCCGACCATGGCAGCGCCAGCTC	900	
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RESULT 8
AX498192 LOCUS 1062 bp DNA linear PAT 26-SBP-2002
DEFINITION Sequence 15 from Patent WO242461.
ACCESSION AX498192
VERSION AX498192.1 GI:23343117
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.
TITLE Endogenous and non-endogenous versions of human g protein-coupled
JOURNAL receptors
Patent: WO 0242461-A 15 30-MAY-2002;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..1062
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/note="Novel Sequence"

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Query Match 93.7%; Score 1048.4; DB 6; Length 1062;
Best Local Similarity 99.9%; Pred. No. 1.6e-251;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGAGCACAGCAGCCGACCTCGCAGCAACAGCTCGCTGCTTGGTGGTCCCGGC 60
Db 1 ATGGAGCACAGCAGCCGACCTCGCAGCAACAGCTCGCTGCTTGGTGGTCCCGGC 60
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Db 1021 CAGTATGACAAAATGGAACCTTATAAA 1050

RESULT 9
BD103852 LOCUS 1062 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel G protein-coupled receptor and its DNA.
ACCESSION BD103852
VERSION BD103852.1 GI:22649426
KEYWORDS WO 0194582-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Terao, Y., Matsui, H. and Shintani, Y.
Novel G protein-coupled receptor and its DNA
Patent: WO 0194582-A 4 13-DEC-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUKO TERAO, HIDEKI MATSUI, YASUSHI SHINTANI
OS Homo sapiens (human)
PN WO 0194582-A/4
PD 13-DEC-2001
PR 02-JUN-2000 JP 00P 170446, 23-JUN-2000 JP 00P 194926 PI
YASUKO TERAO, HIDEKI MATSUI, YASUSHI SHINTANI
PC C12N15/12, C12P21/02, C07K14/705, C07K16/28, A61K45/00, A61P25/00,
PC A61P29/00,
PC A61P09/00, A61P35/00, A61P37/00, A61P1/00, G01N33/566, PC
G01N33/50,
PC G01N33/15
CC Novel G protein-coupled receptor and its DNA
FH Key Location/Qualifiers
FT source 1..1062
/organism='Homo sapiens (human)'
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		Best Local Similarity 99.9%; Pred. No. 1.6e-251;	
		Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	ATGAGCACACGACGCGCCACCTCGCAGCCAAACAGCTCGCTGTCTTGGTGGTCCCGCGC	60
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Qy	61	TGGGCTGGGGCTTGGGTTTCGGCCGGTGTACTACAGCCTCTTGTGTGCTCGGT	120
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Qy	121	TTACGAGCAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAAG	180
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Qy	181	TCTCTCTACAACTATCTCTTGGCACTCGCTGTGCGGACATCTTGGTCTCTTTTCATA	240
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Qy	241	GTGTTGTGGACTTCTCTGTGGAAGATTTCATCTTTGAACATGCAAGTCTCAGTCCGC	300
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Db	301	GACAGATCATAGAGTGTGGAATTCTCATCTATCCATCCACACCTCCATATGATCTGTA	360
Qy	361	CGTTTAAACCATTTGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACCACGCTCTCA	420
Db	361	CGTTTAAACCATTTGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACCACGCTCTCA	420
Qy	421	TACCGAGCCGACCCGGGAAAGTCAATGTAAGTGTATATCACTGTCTTCTGACCAAGC	480
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Qy	481	ATCCCCCTATTACTGTGGCCCAACATCTGGACTGAAGACTACATCAGACCTCTGTGAT	540
Db	481	ATCCCCCTATTACTGTGGCCCAACATCTGGACTGAAGACTACATCAGACCTCTGTGAT	540
Qy	541	CAGCTCTCATCTGGATCCACTGTCTTACCGTCTACCTGGTGGCCCTGTCCATCTTCTTC	600
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Qy	601	ATCTTGAATCAATCATTTGTGTACAGCTCAGGAGGAGCAATTTTGTCTCCGTGGC	660
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Qy	661	TACTCCAGGGGAGAACCCAGCCCATCTTGTTCACCATTTACCTTCATCTTTGGCACTT	720
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Qy	781	TGGCTGGTACATCATGTCCGACATTCGCAATGCTAGCCCTTCTGAAACACAGCCATC	840
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		Best Local Similarity 99.9%; Pred. No. 1.7e-251;	
		Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
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Qy	61	TGGGCTGGGGCTTGGGTTTCGGCCGGTGTACTACAGCCTCTTGTGTGCTCGGT	120
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Qy	121	TTACGAGCAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAAG	180
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Qy	301	GACAGATCATAGAGTGTGGAATTCTCATCTATCCATCCACACCTCCATATGATCTGTA	360
Db	302	GACAGATCATAGAGTGTGGAATTCTCATCTATCCATCCACACCTCCATATGATCTGTA	361
Qy	361	CGTTTAAACCATTTGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACCACGCTCTCA	420
Db	362	CGTTTAAACCATTTGACAGGTATATCTGTCTGCCACCGCTCAAGTACCACGCTCTCA	421
Qy	421	TACCGAGCCGACCCGGGAAAGTCAATGTAAGTGTATATCACTGTCTTCTGACCAAGC	480
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LOCUS CQ867782 2117 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 1 from Patent WO2004074841.
ACCESSION CQ867782
VERSION CQ867782.1 GI:51997901
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Murphy,A.J. and Croll-Kalish,S.
TITLE Kor3l-like proteins and methods of modulating kor3l-mediated
activity
JOURNAL Patent: WO 2004074841-A 1 02-SEP-2004;
REGENERON PHARMACEUTICALS, INC. (US); Murphy, Andrew J. (US);
Croll-Kalish, Susan (US)
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Best Local Similarity 99.9%; Pred. No. 1.8e-251;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAGCAGACGACGCGCCACCTCGAGCAACAGCTCGCTGCTCTTGGTGGTCCCGCGC 60
Db 280 ATGAGCAGACGACGCGCCACCTCGAGCAACAGCTCGCTGCTCTTGGTGGTCCCGCGC 339
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RESULT 12
AX664703 1062 bp DNA linear PAT 22-MAR-2003
LOCUS Sequence 12 from Patent WO02074960.
DEFINITION
ACCESSION AX664703
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VERSION AX664703.1 GI:29164463
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Lei, K.R., Kapeller-Libermann, R. and Glucksmann, M.
TITLE of human proteins and uses thereof
JOURNAL Patent: WO 02074960-A 12 26-SEP-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Query Match 93.0%; Score 1040.4; DB 6; Length 1062;
Best Local Similarity 99.4%; Pred. No. 1.7e-249;
Matches 1044; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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ACCESSION AX664701
VERSION AX664701.1 GI:29164461
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Lei, K.R., Kapeller-Libermann, R. and Glucksmann, M.
TITLE of human proteins and uses thereof
JOURNAL Patent: WO 02074960-A 10 26-SEP-2002;
Millennium Pharmaceuticals, Inc. (US)
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
Smolyar,A., Zhu,Z., Encinas,J., Watanabe,S. and Okigami,H.
Regulation of human chemokine-like receptor
Patent: WO 0348358-A 9 20-JUN-2002;
Bayer Aktiengesellschaft (DE)
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DEFINITION Sequence 23601 from Patent WO02068579.
ACCESSION CQ737667
VERSION CQ737667.1 GI:42336565
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
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thereof
JOURNAL Patent: WO 02068579-A 23601 06-SEP-2002;
PE Corporation (NY) (US)
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Listing first 45 summaries

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7	433.5	22.0	813	8	BZ169352 CH230-259
8	426	21.7	898	9	CNS02ENP Tetraodon
9	414.5	21.1	515	1	AL921815 AL921815

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16	241	12.3	1197	9	AY398777	AY398777 Mus muscu
17	239.5	12.2	1197	9	AY398776	AY398776 Pan trogl
18	238.5	12.1	1197	9	AY398775	AY398775 Homo sapi
C 19	231.5	11.8	1086	9	AY399291	AY399291 Homo sapi
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C 35	213	10.8	1619	3	CR610268	CR610268 full-leng
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DEFINITION t025011ba.r1 TAMBT Bos taurus genomic clone t025011ba, genomic survey sequence.

ACCESSION CC905917
VERSION CC905917.1 GI:33524850

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 803)
AUTHORS Lin,S., Najaf,F.Z., Adelson,D., Gill,C.A. and Roe,B.A.
TITLE Bovine BAC End Sequences from Library TAMBT
JOURNAL Unpublished (2003)
COMMENT Contact: Bruce A. Roe
Advanced Center for Genome Technology
University of Oklahoma Department of Chemistry and Biochemistry
620 Parrington Oval, Room 208, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

Class: BAC ends
High quality sequence start: 39
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FEATURES

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Db 485 CAGCGCAG-CGGGGCAGCGCGGCMCAAGTWCACGCCCTCCGCGCCCTGGGGAGAGC 543
QY 227 ThrAlaIleuPheThrIleThrSerIlePheAlaThrLeuThrAlaProArgIleIle 246
Db 544 ACGGCCATCTGCTGGCCATCACCTCCGCTCTCTCTGCTCTGGCGACCCAGGAGCGTG 603
QY 247 MetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAenArgTyrLeuValHisIleMet 266
Db 604 GTGGTCACTACACCTGTACGTGTAGTGGTTCACACGCGANMTGGCGCTCCACCTGGCC 663
QY 267 SerAspIleAlaAenMetLeuAlaLeuLeuAenThrAlaIleAenPhePheLeuTyrCys 286
Db 664 TAGCACTCTCCACATCTGCGCCATGCTCAACACGCCGCTAACTTCTTCTGTACTGC 723
QY 287 PheIleSerLysArgPheArg 293
Db 724 TTCGTCAAGCAGCGCTTCGC 744

```

RESULT 3

```

CL137737
LOCUS ISB1-110A2 T7.1 ISB1 xenopus tropicalis genomic clone ISB1-110A2,
DEFINITION genomic survey sequence.
ACCESSION CL137737
VERSION CL137737.1 GI:40631372
KEYWORDS GSS.
SOURCE xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
TITLE Xenopodinae; Xenopus; Silurana.
JOURNAL 1 (bases 1 to 824)
COMMENT Krenitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGG
Clas8: BAC ends
High quality sequence start: 2
High quality sequence stop: 672.
Location/Qualifiers
1. :824
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clone="ISB1-110A2"
/clone_lib="ISB1"
/note="Vector: pBelOBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"

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FEATURES

source

```

RESULT 4
A2513631/c 362 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0359L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0359L07 R, genomic survey sequence.
ACCESSION A2513631
VERSION A2513631.1 GI:10694947
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

```

ORIGIN

```

Alignment Scores:
Pred. No.: 1.36e-43 Length: 824
Score: 509.00 Matches: 97
Percent Similarity: 59.51% Conservative: 50
Best Local Similarity: 39.21% Mismatches: 69
Query Match: 25.88% Indels: 31
DB: 9 Gaps: 3

```

```

US-10-689-832-20 (1-372) x CL137737 (1-824)

```

```

QY 27 PheValProValValTyrTyrSerLeuLeuLeuCysLeuGlyLeuProAlaLeuIleLeu 46
Db 157 TTTCTTCTCTACAGT-----AACATGCTG 180

```

```

QY 47 ThrValIleIleLeuSerGlnLeuValAlaArgArgGlnLysSerSerTyrAsnTyrLeu 66
Db 181 ACTGCTGTGGCACTCTCAAGGCTGGCATCGAGACAAGAGTCTCTCTACAGTACCTG 240

```

```

QY 67 LeuAlaLeuAlaAlaAspIleLeuValLeuPheIleValPheValAspPheLeu 86
Db 241 TTGGCTCTTACCATCTCAGACATCTTGAGCCAGATTTTCATCATTTTGTGGGCTTATC 300

```

```

QY 87 LeuGluAspPheIleLeuAenMetGlnMetProGlnValProAspLysIleIleGluVal 106
Db 301 CTGCAACAGACATCTCTCCCGCAAGGTGCCAGTACCTTAATCATCTGGTGTAGTGC 360

```

```

QY 107 LeuGluPheSerSerIleHisThrSerIleThrIleThrValProLeuThrIleAspArg 126
Db 361 CTTGAGTTCTCTCTTAATCATGATCTATTTGGGTGACAGTATGATCTGACCGTGGACCT 420

```

```

QY 127 TyrIleAlaValCysHisProLeuLysTyrHisThrValSerTyrProAlaArgThrArg 146
Db 421 TATGTGGCATTTATGTCATCCGCTACATATGCTCTTTCTCTTACCCAGAGCAACCCGT 480

```

```

QY 147 LysValIleValSerValTyrIleThrCysPheLeuThrSerIleProTyrTyrThrTP 166
Db 481 AGAGTCATGTGTTGTCTCTCTCTCCTCCTGTCGCGGTGATACCTTCTTACTGGTGG 540

```

```

QY 167 ProAenIleThrThrGluAspTyrIleSerThrSerValHisValleuIleThrIle 186
Db 541 AGTGATGTTGGAGGATCCGCTACCCAGGATGCTAGACCTTATCTCAAGTGGACC 600

```

```

QY 187 HisCysPheThrValTyrLeuValProCysSerIlePheIleLeuAenSerIleIle 206
Db 601 CACTGCTTTATAATATATCTTCTATCCCTGCACCATATTTTGTATACCACTCTGTCATT 660

```

```

QY 207 ValTyrLysLeuArgArgLysSer-----AsnPheArgLeuArgGly 220
Db 661 ATCTACAGGCTGAGGAGAAAGAACAGAGGGTCCAGAAATGCGACCTTTCCTTAATGGGC 720

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```

QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 721 AAGACCCACAGCAATTTCTCCGGGGCATTAACCTCTGTTTTTTTGGCCGGTTCCTTT 780

```

```

QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAenArg 260
Db 781 TGG-----GGCCTCCCTTAAAAAAACCCAT 804

```

```

QY 261 -TrpLeuValHisIleMet 266

```

```

Db 805 TTGGTCCATCCATTAAATT 823

```

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Db 72 TACTCCCTCCGCCACCTCTCGGGGGCGGGCGCTGTCGACATTCCTCACCGATCTT 131
 Qy 270 AlaAsnMetLeuAlaLeuLeuAsnThrAlaIleAsnPhelLeuValPheValaspPheLeu 86
 Db 132 GCCAACATGTGGGTGCTCAACACGGGTGTTAACTTCTCTCTACTGTTTCATCAGC 191
 Qy 290 LysArgPheArgThrMetAlaAlaAlaThrLeuLysAlaPhePheLysCysGlnLysGln 309
 Db 192 WAGCGTTTCGGGGCATGGCGGCCAACGCTGCTCGAGCGCTGCTCCACTGCAGGAAGCAG 251
 Qy 310 ProValGlnPheThrThrAsnHisAsnPhelSerIleThrSerSerProThrIleSerPro 329
 Db 252 CTGACCGCTTCTACGCCAGCACAACTTTTCATCAGAGTGCCTCCGCTGCTCAACA 311
 Qy 330 AlaAsnSerHisCysIleLysMetLeuValTyrglnTyrglnTyrglnTyrglnTyrgln 349
 Db 312 GCAACTCCCACTGCATCAAGATGCTGTGTACCACTAGCAGACAAACCGGGAAGCCATC 371

RESULT 6

CL137848
 LOCUS 1 ISB1-110C15 T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-110C15,
 genomic survey sequence.
 CL137848 1 GI:40631483

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 Xenopodinae; Xenopus; Silurana.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 867)
 Mardis, E. and Wilson, R.
 A physical map of the xenopus tropicalis genome
 Unpublished (2003)
 Contact: Richard K Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 75000 Std Error: 0.00
 Seq primer: T7 TAATACGACTCACTATAGG
 Class: BAC ends
 High quality sequence start: 11
 High quality sequence stop: 673.

FEATURES

source

1..867
 /organism="Xenopus tropicalis"
 /mol_type="genomic DNA"
 /db_xref="taxon:8364"
 /clone="ISB1-110C15"
 /clone_lib="ISB1"
 /note="Vector: pBelOBAC11; ISB-1 Xenopus tropicalis BAC
 Library Segment 1"

ORIGIN

Alignment Scores:
 Pred. No.: 1,34e-36 Length: 867
 Score: 444.00 Matches: 92
 Percent Similarity: 61.06% Conservative: 46
 Best Local Similarity: 40.71% Mismatches: 62
 Query Match: 22.57% Indels: 26
 DB: 9 Gaps: 4

US-10-689-832-20 (1-372) x CL137848 (1-867)

Qy 27 PheValProValValTyrglnTyrglnTyrglnTyrglnTyrglnTyrglnTyrglnTyrgln 46
 Db 172 TTCTCTCTCTACAGT-----ACATGCTG 195
 Qy 47 ThrValIleIleLeuSerGlnLeuValAlaArgArgGlnLysSerSerTyrglnTyrgln 66
 Db 196 ACTGCTGTGGCACTCTCAAGGCTGCATCGAGAACAAAGAGTCTCTCTACAGTTACCTG 255

Qy 67 LeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIleValPheValaspPheLeu 86
 Db 256 TTGGCTCTTACCATCTCAGACATCTTGAGCCAGATTTTCATCATCTTTTGGGCTTATC 315
 Qy 87 LeuGluAspPheIleLeuAsnMetGlnMetProGlnValProAspLysIleIleGluVal 106
 Db 316 CTCGAACAGCAATACTCCACGCAAGGTGCCCTTAATCCATCGTGTGCTGTCAGTGC 375
 Qy 107 LeuGluPheSerSerIleHisThrSerIleTrrIleThrValProLeuThrIleAspArg 126
 Db 376 CTTGAGTTCTCTCTAATCATGCATCTATTGGGTGACAGTGATGATGACCGTGGACCGT 435
 Qy 127 TyrIleAlaValCysHisProLeuLysTyrglnHisThrValSerTyrglnAlaArgThrArg 146
 Db 436 TATGTGGCATATGCTATCGCTACAATATCGCTCTTCTCTTACCAGAGCAACCGT 495
 Qy 147 LysValIleValSerValTyrglnTyrglnTyrglnTyrglnTyrglnTyrglnTyrgln 166
 Db 496 AGAGTCATTTGCTTCT 555
 Qy 167 ProAsnIleTrrThrGluAspTyrglnSerThrSerValHisValLeuIleTrrIle 186
 Db 556 AGTGATGTTGGAGGATCCGCGTATCCAGGATGCTAGACCTTATATCTCAAGTGGACC 615
 Qy 187 HisCysPheThrValTyrglnLeu--ValProCysSerIlePhePheIleLeuAsnSerIle 206
 Db 616 CACTGCTTTAATAATATATCTTCCATCTCCCTCGACCATATTTTTCATTAACCAACTCTG 675
 Qy 206 LeValTyrgln-----LysLeuArgArgLysSer-----Asp 216
 Db 676 GTCAATATCTTACCAGGCTGAGGAAAAAAGCGGGTCCCAAGGAAGTTGCCCATCTCT 735
 Qy 216 HeArgLeuArgGlyTyrglnSerThrGlyLysThrAlaIleLeuPheThrIleThrSerI 236
 Db 736 TTCCTAAATGGGCCAAGAA-----CCACACAGTCAATTTCTTCTTCTTTGGAGACAA 789
 Qy 236 LePheAlaThrLeu 240
 Db 790 TTATACCTCTCCCTG 803

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 259 row: E column: 22
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source
 1. .813
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-259E22"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Alignment Scores:
 Pred. No.: 1.62e-35 Length: 813
 Score: 433.50 Matches: 90
 Percent Similarity: 88.57% Conservative: 3
 Best Local Similarity: 85.71% Mismatches: 5
 Query Match: 22.04% Indels: 7
 DB: 8 Gaps: 1

US-10-689-832-20 (1-372) x BZ169352 (1-813)

QY 37 LeuCysLeuGly-----LeuProAlaAsnIleLeuThrValIle 49
 DB 499 CTTTGCTTGGGATACTTTGATCTCTCTCCACAGCAGATATCTTGACAGTCATC 558
 QY 50 IleLeuSerGlnLeuValAlaArgGlnLysSerTyrAsnTyrLeuLeuAlaLeu 69
 DB 559 ATCTCTCTCAACTGGTACGAGAGAGACAGAGTCTCTCAACTATCTTCTGCACTT 618
 QY 70 AlaAlaAlaAspIleLeuValLeuPhePheIleValPheValAspPheLeuGluAsp 89
 DB 619 GCTGTCGCGACATCTGGTCTCTTTTTCATCGCTTTGTGGATTTCTTGTAGAAGAC 678
 QY 90 PheIleLeuAsnMetGlnMetProGlnValProAspLysIleIleGluValLeuGluPhe 109
 DB 679 TTCATTGTGACCATGACATGCTCCGATCCCTGACAGATCATAGAGTCTAGAGTTC 738
 QY 110 SerSerIleHisThrSerIleTrpIleThrValProLeuThrIleAspArgTyrIleAla 129
 DB 739 TCCTCCATCCACACTTCTATTGTGATTACAGTCCCTTAAACAGTTGATAGGTATATCGCA 798
 QY 130 ValCysHisProLeu 134
 DB 799 GTCTGTCAACCCACTC 813

RESULT 8

CNS02ENP 898 bp DNA linear GSS 01-SEP-2000
 LOCUS Tetraodon nigroviridis genome survey sequence, PUC-ori end of clone
 DEFINITION 262F08 of library G from Tetraodon nigroviridis, genomic survey
 sequence.

ACCESSION

VERSION AL193966.1 GI:7832072

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Estimate of human gene number provided by genome-wide analysis

TITLE

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

JOURNAL

TITLE

JOURNAL

COMMENT

JOURNAL

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TITLE

using Tetraodon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)

20296633
 10835645

Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
 Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
 Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837
 10899143

3 (bases 1 to 898)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetraodon>.

Location/Qualifiers

1. .898

/organism="Tetraodon nigroviridis"

/mol_type="genomic DNA"

/db_xref="taxon:99883"

/clone="262F08"

/clone_lib="G"

/note="Genoscope sequence ID : COAG262DC04SP1-end :
 PUC-ori"

Alignment Scores:
 Pred. No.: 1.19e-34 Length: 898
 Score: 426.00 Matches: 76
 Percent Similarity: 67.65% Conservative: 39
 Best Local Similarity: 44.71% Mismatches: 55
 Query Match: 21.66% Indels: 1
 DB: 9 Gaps: 0

US-10-689-832-20 (1-372) x CNS02ENP (1-898)

QY 42 ProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAArgGlnLysSer 61

DB 373 CCATGAACATCTTCGCGGTGACGGTCCGCGTGGCGTCCCGCACCAGAGGCA 432

QY 62 SerTyrAsnTyrLeuLeuAlaAlaAlaAspIleLeuValLeuPheIleVal 81

DB 433 CTGTACTACTACTGCTGGCGGTGACAGGCTCCGACATCTCTCCAGCTCTTCATCATC 492

QY 82 PheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValProAsp 101

DB 493 TTCGTGGGCTTCTGTGTGGAGACGCGATTTTCCACCGGAGGTCCTCGCTCTCTTA 552

QY 102 LysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrValPro 121

DB 553 CACTCAGTCAGCGCGCGAGTTTGGCGCGAACACGCTCCATCTGTGTCACCGTCCCC 612

QY 122 LeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSerTyr 141

DB 613 CTCACGTTGGACCGCTAGTGGCGGTGGCCACCCCTCTCCACAGCAGATCAGTAC 672

QY 142 ProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSerIle 161

DB 673 CCGGCGCGGACAGAGGATCATCGGTGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGT 732

QY 162 ProTyrTyrTrpTrpProAsnIleThrGluAspTyrIleSerThrSerValHis 181

DB 733 CCCCTTCTTCTGTGTCGATGCGAGGAGAACAGCCCGCCGACCGS-CTGAGAGCG 791

QY 182 ValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePheIle 201

```

Db      792  GTCCTCATCTGGACCCACCTGACCATCATCTCTCTGCTGCGACGATCTTCTCGGTC 851
Qy      202  LeuAsnSerIleIleValTyrLysLeuArg 211
Db      852  CTCACACTCTTGCATCATCCACGCTGAGG 881

RESULT 9
LOCUS   AL921815
DEFINITION AL921815 PUR-21+22 Danio rerio cDNA clone 101-F03-2, mRNA sequence.
ACCESSION AL921815
VERSION   AL921815.1 GI:23188395
KEYWORDS EST.
SOURCE   Danio rerio (zebrafish)
ORGANISM Danio rerio
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
          Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 515)
AUTHORS   Lo, J., Lee, S., Xu, M., Liu, F., Ruan, H., Eun, A., He, Y., Ma, W.,
          Wang, W., Wen, Z., and Peng, J.
          15000 unique zebrafish EST clusters and their future use in
          microarray for profiling gene expression patterns during
          embryogenesis
JOURNAL   Genome Res. 13 (3), 455-466 (2003)
MEDLINE   22505427
PUBMED    12618376
COMMENT   Contact: Peng J
          Lab of Functional Genomics
          Institute of Molecular and Cell Biology
          30 Medical Drive, Singapore, 117609, Singapore
          Email: pengj@imcb.a-star.edu.sg
          Clone requests: info@openbiosystems.com
          Open Biosystems,
          6705 Odyssey Drive, Huntsville, AL 35806.
          Location/Qualifiers
FEATURES
     source
         1..515
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             /mol_type="mRNA"
             /strain="local wildtype"
             /db_xref="taxon:7955"
             /clone="101-F03-2"
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             /clone_lib="PUR-21+22"

ORIGIN
Alignment Scores:
Pred. No.:      9.03e-34      Length:      515
Score:          414.50      Matches:    104
Percent Similarity: 37.46%      Conservative: 14
Best Local Similarity: 33.02%      Mismatches: 29
Query Match:    21.07%      Indels:     168
DB:             1           Gaps:         4

US-10-689-832-20 (1-372) x AL921815 (1-515)

Qy      1  MetGluHisThrHisAlaHisLeuAlaAAsnSerSerLeuSerTyrTrpSerProGly 20
Db      60  ATAGAGCAGCAGCCATCTTCCACGTCGTGACCAACCACTCCAGCTCTCGAGCCCT--- 116
Qy      21  SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db      117  CGCGGTGTCTCTGGACAGTTTCAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 176
Qy      41  LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAArgGlnLys 60
Db      177  CTGCAGCAACATCTCTCAGCGTATCATCTTCTCAGCTG----- 218
Qy      61  SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAAspIleLeuValLeuPhePheIle 80
Db      218  ----- 218

```

```

Qy      81  ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db      218  ----- 218
Qy      101  AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
Db      218  ----- 218
Qy      121  ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db      218  ----- 218
Qy      141  TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db      218  ----- 218
Qy      161  IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
Db      218  ----- 218
Qy      181  HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db      218  ----- 218
Qy      201  IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPhe-ArgLeuArgGln 220
Db      219  -----CTCCCGCTCCGAGG 233
Qy      220  YTrsSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrIle 240
Db      234  ATACTCGACCGGAAAGACACCGCTATCTCTTTAGCCATCACCTCAGTGTTCGCGCTTTT 293
Qy      240  uTrpAlaProArgIleIleMetIleLeuTyrHisLeuTyr-----GlyAlaPro 256
Db      294  ATGGCGGCTCTACACTATGATCTTTATCATCTTTACAGGTGCAACAGCGATGCC 353
Qy      256  oileGlnAsnArgTrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLe 276
Db      354  GGGTCGCGCTAGA---CTCCTGCATTTGGTAACGGATGTAGCGAACATGCTTGTCTACT 410
Qy      276  uAsnThrAlaIleAsnPheLeuTyrCysPheIleSerLysArgPheArgThrMetAl 296
Db      411  CAACACCGGGGTCAACTTCTCTCTACTGCTTTATAAGCAAGCGCTTTTCGGAGGATGCG 470
Qy      296  aAlaAlaThrLeuLysAlaPhePheLysCysGlnLysGlnPro 310
Db      471  CGGGACGGTGCTCAAAAGCCTTTTTCGCTGCAGAAACAGCCG 513

RESULT 10
LOCUS   AQ225693/c
DEFINITION HS_2009_B2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=16 Row=D, genomic survey sequence.
ACCESSION AQ225693
VERSION   AQ225693.1 GI:3650922
KEYWORDS GSS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 448)
REFERENCE Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
          Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
          Hood, L.
          Sequence-tagged connectors: A sequence approach to mapping and
          scanning the human genome
          Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL   99380589
MEDLINE   1049764
PUBMED
COMMENT   Contact: Mahairas GG, Wallace JC, Hood L
          High Throughput Sequencing Center

```

University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2009 row: D column: 16
Class: BAC ends
High quality sequence stop: 448.

FEATURES

source

Location/Qualifiers
1..1269

/organism="Gasterosteus aculeatus"

/mol_type="genomic DNA"

/strain="Salmon River"

/db_xref="taxon:69293"

/clone="CH213-237F13"

/sex="Mixed"

/cell_type="Blood"

/clone_lib="CH213"

/note="Vector: pTARBAC2.1; Site 1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (<http://cegs.stanford.edu>). The clone was isolated from the BAC library CHORI-213 built by Pieter deJong in collaboration with the Stanford Genome Evolution Center (<http://www.chori.org/bacpac/>). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm)."

ORIGIN

US-10-689-832-20 (1-372) x A0225693 (1-448)

Alignment Scores:

Pred. No.: 5.51e-32 Length: 448
Score: 397.00 Matches: 74
Percent Similarity: 95.12% Conservative: 4
Best Local Similarity: 90.24% Mismatches: 4
Query Match: 20.18% Indels: 0
DB: 8 Gaps: 0

ORIGIN

Qy 269 IleAlaAnMetLeuAlaLeuLeuAnThrAlaIleAnPhePheLeuTyrcysPheIle 288
Db 435 ATAGCAACAGTGATAGCCCTTGAGCAGCAGCCATCAACTTCTCTATATCTGGCTCATC 376
Qy 289 SerLysArgPheArgThrMetAlaAlaAlaThrLeuLysAlaPhePheLysCysGlnLys 308
Db 375 AGCAAGCGGTTCGACCATCGCCAGCCAGCTCAAGGCTTCTTCAAGTGCCAGAG 316
Qy 309 GlnProValGlnPheTyThrAsnHisAnPheSerIleThrSerSerProThrIleSer 328
Db 315 CACCNTGTACAGTTCTACACCAATCATTAACATTTTCCATAACAAGTAGCCCTGGATCTCG 256
Qy 329 ProAlaAnSerHisCysIleYsMetLeuValTyGlnTyArgLysAsnGlyLysPro 348
Db 255 CCGGCAAACTCAGTGTACATCAAGATGCTGGTGATACCATGATGACAAAATGGAACCT 196
Qy 349 IleLys 350
Db 195 ATAAAA 190

RESULT 11

CL649540

LOCUS

DEFINITION CH213-237F13 SP6 CH213 Gasterosteus aculeatus genomic clone

CH213-237F13 3', genomic survey sequence.

ACCESSION

CL649540

VERSION

CL649540.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Gasterosteus aculeatus (three spined stickleback)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;

Gasterosteidae; Gasterosteus.

1 (bases 1 to 1269)

Kingsley, D., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.

Expressed sequence tags from Gasterosteus aculeatus

Unpublished (2004)

Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Avenue, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@hgsc.stanford.edu

Plate: 237

Class: BAC ends

High quality sequence start: 19

High quality sequence stop: 869.

FEATURES

source

Location/Qualifiers

1..1269

/organism="Gasterosteus aculeatus"

/mol_type="genomic DNA"

/strain="Salmon River"

/db_xref="taxon:69293"

/clone="CH213-237F13"

/sex="Mixed"

/cell_type="Blood"

/clone_lib="CH213"

/note="Vector: pTARBAC2.1; Site 1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (<http://cegs.stanford.edu>). The clone was isolated from the BAC library CHORI-213 built by Pieter deJong in collaboration with the Stanford Genome Evolution Center (<http://www.chori.org/bacpac/>). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm)."

ORIGIN

Alignment Scores:
Pred. No.: 1.15e-29 Length: 1269
Score: 381.50 Matches: 76
Percent Similarity: 70.71% Conservative: 23
Best Local Similarity: 54.29% Mismatches: 25
Query Match: 19.40% Indels: 17
DB: 9 Gaps: 3

US-10-689-832-20 (1-372) x CL649540 (1-1269)

Qy 246 IleMetIleLeuTyrcysPheIleLeuValHisLeuValHisLeuValHisLeu 265
Db 11 GTTTTACTCCGCCGCCGCTTTCACGGGCGCGCGG-CGA-----CTGCTCCACGTG 60
Qy 266 MetSerAspIleAlaAnMetLeuAlaLeuLeuAnThrAlaIleAnPhePheLeuTyrcys 285
Db 61 CTCACCGACCTTGGCCATATGCTCGGTGCTCAACCCGGGGTCAACTTCTTCTTTAC 120
Qy 286 CysPheIleSerLysArgPheArgThrMetAlaAlaAlaThrLeuLysAlaPhePheLys 305
Db 121 TGTCTTCATCAGACGCTTTCGCGGCATGCGGCCAACGCTCTGCGGGCCCTGGTCAAC 180
Qy 306 CysGlnLysGlnProValGlnPheTyThrAsnHisAnPheSerIleThrSerSerPro 325
Db 181 TGCAGGAGCAGCAGCGCGCGCTTCTACGCCAGCCACACACTTTCATCAGCAGCGCG 240
Qy 326 TrpIleSerProAlaAnSerHisCysIleLysMetLeuValTyGlnTyAspLysAsn 345
Db 241 TGGATCTCAGCGGCCACTCCCACTGCATTAAAGATGCTGGTGATGACAGTATGACAAAAT 300
Qy 346 GlyLysProfile-----LysSerArgAsnAspSer 355
Db 301 GGGAAACCCGCTGTATTTCTCTTGGTCTCTCAGCCACAGCGGCGGCGCGCGCG 360
Qy 356 -----LysSerSerTyrcysPheGlnPheGlnAspAlaIleGlyAlaCysValleIleLeu 372
Db 361 CCTCTCCCGCCGACCTCTCTCCCTCACCCCTCAGTGTGTGGGGCGGCACATTTCTCTT 420

RESULT 12

BU610327

LOCUS

DEFINITION

UI-M-DJ2-bw1-f-07-0-UI.r1 NIH BMAP DJ2 Mus musculus cDNA clone

UI-M-DJ2-bw1-f-07-0-UI 5', mRNA sequence.

ACCESSION

BU610327

708 bp mRNA linear EST 20-FEB-2003

Db	123	TGGATCTCACCAGCAAACTCACTGCATCAAGATGCTGGTGTACCAAGTATGACAACAT	102
QY	346	GlytysProfileLys 350	
Db	183	GGAAAGCCTATATAA 197	
RESULT 13			
AQ344035/c			
LOCUS			
DEFINITION			
ACCESSION	AQ344035		
VERSION	AQ344035.1	GI:4168931	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	1 (bases 1 to 588)		
TITLE	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.		
JOURNAL	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready		
COMMENT	Map Building Unpublished (1997) Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buhalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buhalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: T7 Class: BAC ends.		
FEATURES			
source	Location/Qualifiers		
	1..588		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="GDB:7547470"		
	/db_xref="taxon:9606"		
	/clone="RPCI-11-124J23"		
	/sex="Male"		
	/cell_type="Lymphocytes"		
	/clone_lib="RPCI-11"		
	/note="Vector: pBACs3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"		
ORIGIN			
Alignment Scores:			
Pred. No.:	6.32e-23	Length:	588
Score:	314.00	Matches:	66
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	15.96%	Indels:	0
DB:	8	Gaps:	0
US-10-689-832-20	(1-372) x AQ344035	(1-588)	
QY	43	AlaasnlleleuthrValilleleLeuserGlnleuValAlaAargGlnLysSerSer	62
Db	199	GCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAGTCTCTCC	140
QY	63	TyrAsnTyrlleuLeuAlaLeuAlaAlaAspIleuValleuPheIleValPhe	82
Db	139	TACAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTGGTCTCTCTTTTCATAGT	80
QY	83	ValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValProAspLys	102

```

Db      79 GTGACTTCCTGTTGGAAGATTTCATCTTGAACATGCAGATGCCTCAGGTCCTCCCGACAAG 20
Qy      103 lleleGluValLeuGlu 108
Db      19 ATCATAGAAGTGCTGGAA 2

RESULT 14
LOCUS   AQ351433/3
DEFINITION   AQ351433 603 bp DNA linear GSS 07-MAY-1999
              RPC111-113113.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-113113,
              genomic survey sequence.
ACCESSION   AQ351433
VERSION     AQ351433.1 GI:4178768
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 603)
AUTHORS     Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and
            Venter,J.C.
TITLE       Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
JOURNAL     Unpublished (1997)
COMMENT     Other GSSs: RPC111-113113.TV
            Contact: Shaying Zhao, William Niernan, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@reagen.com). BAC end search page:
            http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
            Seq primer: SP6
            Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..603
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7543212"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-113113"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPC111 Human Male BAC Library"

ORIGIN
Alignment Scores:
Pred. No.:          2.25e-22      Length:          603
Score:              309.00        Matches:          65
Percent Similarity: 100.00%      Conservative:    0
Best Local Similarity: 100.00%  Mismatches:         0
Query Match:        15.71%       Indels:           0
DB:                  8            Gaps:              0

US-10-689-832-20 (1-372) x AQ351433 (1-603)

Qy      43 AlaAniLeuThrValIleLeuSerGlnLeuValAlaArgArgGlnLysSerSer 62
Db      195 GCATATATCTTGACAGTGTATCATCTCTCCAGCTGGTGGCAAGACAGAGTCTCTCC 136

Qy      63 TyrAnfYrLeuLeuAlaLeuAlaAlaLeuValLeuValLeuPheIleValPhe 82
Db      135 TACAACATATCTCTGGCACTCGCTGCTGCCGACATCTTGGTCTCTCTTTTCATAGTGT 76

Qy      83 ValaapPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValProAspLys 102

```

```

Db      75 GTGACTTCCTGTTGGAAGATTTCATCTTGAACATGCAGATGCCTCAGGTCCTCCCGACAAG 16
Qy      103 lleleGluValLeu 107
Db      15 ATCATAGAAGTGCTG 1

RESULT 15
LOCUS   CNS04L7F
DEFINITION   CNS04L7F 1107 bp DNA linear GSS 01-SEP-2000
              Tetraodon nigroviridis genome survey sequence T7 end of clone
              118A07 of library G from Tetraodon nigroviridis, genomic survey
              sequence.
ACCESSION   AL295764
VERSION     AL295764.1 GI:8034344
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
ORGANISM    Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Bizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE       Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
JOURNAL     Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE     20296633
PUBMED      10835645
REFERENCE   2
AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
TITLE       Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL     Genome Res. 10 (7), 939-949 (2000)
MEDLINE     20359837
PUBMED      10899143
REFERENCE   3 (bases 1 to 1107)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/tetraodon.
            Location/Qualifiers
            1..1107
            /organism="Tetraodon nigroviridis"
            /mol_type="genomic DNA"
            /db_xref="taxon:99883"
            /clone="118A07"
            /clone_lib="G"
            /note="Genoscope sequence ID : COBGL18AA04LP1-end : T7"

ORIGIN
Alignment Scores:
Pred. No.:          1.45e-15      Length:          1107
Score:              249.00        Matches:          41
Percent Similarity: 81.43%      Conservative:    16
Best Local Similarity: 58.57%  Mismatches:         13
Query Match:        12.66%       Indels:           0
DB:                  9            Gaps:              0

US-10-689-832-20 (1-372) x CNS04L7F (1-1107)

Qy      224 GlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeuTrpAlaPro 243
Db      71 GGGAGAGACAGCGCCATGCTCTGCCCATCACCTCCGTCCTCTCTGTGCTCTGGGACCC 130

```

```

Qy 244 ArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArgTrrLeuVal 263
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131 AGGACGGTGGTGGTCACTACCACTGTACGTGTGGTGGTTCACCGCGGACTGGCGGTC 190
Qy 264 HisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIleAsnPhePhe 283
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 CACCTGGCCTACGACCTGTCCAACATGCTGGCCATGCTCAACACGGCGGCTCAACTTCTTC 250
Qy 284 LeuTyrCysPheIleSerLysArgPheArg 293
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 CTGTACTGCTTCGTACGACGCGGTTCCGC 280

```

Search completed: February 12, 2005, 15:53:21
Job time : 3095 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2005, 18:10:52 ; Search time 164 Seconds
(without alignments)
877.286 Million cell updates/sec

Title: US-10-689-832-20

Perfect score: 1967

Sequence: 1 MEHTHAHLAANSLSWSPG.....NDSKSSYQFEDAIGACVIL 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1967	100.0	372	4	Aau10067 Chemokine
2	1967	100.0	372	5	Aae18645 Human G-p
3	1967	100.0	372	6	Abre2521 Human G-p
4	1967	100.0	372	7	Add18023 Human G-p
5	1967	100.0	372	7	Adj87767 G-coupled
6	1967	100.0	372	8	Adi79323 NOVI0a pr
7	1962	99.7	372	8	Ados6002 Human NOV
8	1939.5	98.6	369	6	Abre2522 Human G-p
9	1864	94.8	591	7	Adf70485 Orphan re
10	1857	94.4	353	5	Aau76416 Novel G-p
11	1857	94.4	353	5	Abj04075 Human G p
12	1857	94.4	353	5	Abp79517 Human che
13	1857	94.4	353	6	Abp98724 Human AXO
14	1857	94.4	353	6	Abp44437 Human G p
15	1857	94.4	353	6	Abbr2499 Human TGR
16	1857	94.4	353	8	Adri16434 Human KOR
17	1853	94.2	353	4	Aau10068 Chemokine
18	1853	94.2	353	7	Adj87769 G-coupled
19	1853	94.2	353	8	Adi79325 NOVI1 pro
20	1853	94.2	353	8	Ados6004 Human NOV
21	1853	94.2	353	8	Ado28954 Human nov
22	1829	93.0	353	5	Aae29236 Human TTM
23	1829	93.0	353	6	Abg71163 Novel hum
24	1829	93.0	353	6	Abu09571 Human pro
25	1741	88.5	345	6	Abb2508 Mouse TGR

26	1741	88.5	345	8	ADO28956	Ado28956 Mouse nov
27	1628	82.8	318	7	ADJ87772	Adj87772 G-coupled
28	1628	82.8	318	8	ADI79348	Adi79348 NOVI0b pr
29	1628	82.8	318	8	ADO56027	Ado56027 Human NOV
30	1623	82.5	333	5	AAE17081	Aae17081 Human G-p
31	1623	82.5	333	7	ABW00814	Abw00814 Human GPC
32	1623	82.5	343	5	ABB79519	Abb79519 Human che
33	1623	82.5	356	5	ABB79518	Abb79518 Human che
34	1623	82.5	385	5	ABP95606	Abp95606 Human GPC
35	1623	82.5	388	8	ADQ89946	Adq89946 Antagonis
36	1611	81.9	333	5	AAE17229	Aae17229 Human thy
37	1471	74.8	287	4	AAU25559	Aau25559 Human G p
38	1421	72.2	321	7	ADC12696	Adc12696 Human GPC
39	1317	67.0	265	6	ABP81706	Abp81706 Human G p
40	1317	67.0	265	6	ABR62524	Abre62524 Human G-p
41	912.5	46.4	313	4	AAU25556	Aau25556 Human G p
42	742	37.7	340	8	ADO28936	Ado28936 Mouse nov
43	742	37.7	348	6	ABR82431	Abre82431 Murine is
44	737	37.5	374	5	ABJ04070	Abj04070 Human G p
45	737	37.5	374	5	AAM49155	Aam49155 Human G p

ALIGNMENTS

RESULT 1

AAU10067

ID AAU10067 standard; protein; 372 AA.

AC AAU10067;

XX

DT 14-FEB-2002 (first entry)

XX

DE Chemokine receptor family related protein, NOVI0.

XX

KW NOV; cytostatic; psoriasis; nootropic; neuroprotectant; cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia; haemostatic; atherosclerosis; gene therapy; neurogenesis; motility; differentiation; proliferation; haematopoiesis; wound healing; angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis; haemophilia; allergy; Pendred syndrome; skeletal dysplasia; ischaemic injury; neuroepithelial disorder; hepatitis; heart failure; chemokine receptor; chromosome 1.

XX Homo sapiens.

OS

XX

PH Location/Qualifiers

FT Peptide

FT I.:47 /label= Signal_peptide

FT Protein

FT 48..372 /note= "Mature chemokine receptor related protein, NOVI0"

XX

XX WO200170978-A2.

PD

XX 27-SEP-2001.

XX

XX 20-MAR-2001; 2001WO-US009093.

XX

XX 20-MAR-2000; 2000US-0190768P.

XX

XX 20-MAR-2000; 2000US-0190835P.

XX

XX 22-MAR-2000; 2000US-0190972P.

XX

XX 22-MAR-2000; 2000US-0191199P.

XX

XX 24-MAR-2000; 2000US-0191947P.

XX

XX 28-MAR-2000; 2000US-0192657P.

XX

XX 28-MAR-2000; 2000US-0192664P.

XX

XX 28-MAR-2000; 2000US-0192665P.

XX

XX 28-MAR-2000; 2000US-0192984P.

XX

XX 29-MAR-2000; 2000US-0192984P.

XX

XX 31-MAR-2000; 2000US-0193843P.

XX

XX (CURA-) CURAGEN CORP.

XX

XX Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;

XX

PI Vernet CAM;
XX WPI: 2001-639127/73.
DR N-PSDB; AAS15730.
XX Polypeptides and nucleic acids related to chloride channel, insulin-like
PT growth factor family of proteins, useful for diagnosing and treating
PT cancer, cystic fibrosis, acute pancreatitis and Alzheimer's disease.
XX
XX Claim 1; Page 42; 151pp; English.
XX
CC The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX
CC polypeptides are useful for treating pathology associated with NOVX
CC polypeptide, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX, identifying agents binding to
CC NOVX and treatment of disorders associated with altered expression of
CC members of chloride channel-associated proteins e.g. cystic fibrosis and
CC congenital myotonia. NOVX proteins are useful in treatment of disorders
CC including psoriasis, cancer, diabetes, metabolic disorders of pancreas,
CC e.g. acute pancreatitis, abnormal growth and accumulation of mast cells
CC in one or more organs (e.g. haemophilia, anaemia), Pendred syndrome,
CC skeletal dysplasias, disorders characterised by altered cell shape,
CC motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial
CC disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the
CC treatment of disorders of vascular smooth muscle cell differentiation,
CC (e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are
CC useful to screen for molecules which inhibit or enhance NOVX activity or
CC function and are useful as targets for the identifying small molecules,
CC that modulate or inhibit e.g. neurogenesis, proliferation, motility, cell
CC differentiation, haematopoiesis, wound healing and angiogenesis. NOV
CC sequences are also useful for: identifying a cell or tissue type in a
CC biological sample; amplifying DNA sequences from very small biological
CC samples e.g. hair or skin or body fluids and as primers and probes to
CC identify and/or clone NOVX homologues. NOVX proteins are useful
CC immunogens to generate antibodies to monitor protein levels and modulate
CC NOVX activity. Cells comprising the nucleic acids are useful for
CC producing transgenic animals, for studying the function and/or activity
CC of NOVX protein and identifying and/or evaluating modulators of NOVX
CC protein activity. This sequence is the NOV10 amino acid sequence (gene
CC located on chromosome 1) related to the chemokine receptor family of
CC proteins, one of 12 NOV polypeptides described in the method of the
XX invention
XX
SQ Sequence 372 AA;
Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. NO. 1.2e-209;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANSSLSWSPGSCAGLGFVPVYVYSLLCGLPANILTVIILSOLVARRQK 60
DB 1 MEHTAHLAANSSLSWSPGSCAGLGFVPVYVYSLLCGLPANILTVIILSOLVARRQK 60
QY 61 SSVNYLLAALADILVLFVFDLLEDFILNMOMQVPDKIEVLEPSSHTSIWTV 120
DB 61 SSVNYLLAALADILVLFVFDLLEDFILNMOMQVPDKIEVLEPSSHTSIWTV 120
QY 121 PLTDRIYIACHPLKHTVSPARTKVIUSVYITCFILSPYIYWNPNWTEDIYSTSVH 180
DB 121 PLTDRIYIACHPLKHTVSPARTKVIUSVYITCFILSPYIYWNPNWTEDIYSTSVH 180
QY 181 HVLINWCHTIVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSFATL 240
DB 181 HVLINWCHTIVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINFLFYCFISKRFRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINFLFYCFISKRFRTMAAATL 300
QY 301 KAFFKQKQVPQVFTYNNHNSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSVQ 360
DB 301 KAFFKQKQVPQVFTYNNHNSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSVQ 360

QY 361 FEDAIGACVIL 372
DB 361 FEDAIGACVIL 372
RESULT 2
AAE18645
XX AAE18645 standard; protein; 372 AA.
AC AAE18645;
XX
DT 17-MAY-2002 (first entry)
DE Human G-protein coupled receptor (GCRC-6).
XX
KW Human; G-protein coupled receptor; GCRC-6; cell proliferative disorder;
KW neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;
KW metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease; hypertension;
KW atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic;
KW osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening;
KW transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant;
KW neurotic; neuroprotective; cardiant; immunosuppressive; anorectic;
KW virucide; receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..47
FT Domain /label= Signal_peptide
FT /note= "Transmembrane domain"
FT 32..52
FT Protein 48..372
FT /label= Human_mature_GCRC-6
FT Domain 74..100
FT /note= "Transmembrane domain"
FT 184..208
FT /note= "Transmembrane domain"
XX
PN WO200210387-A2.
XX
PD 07-FEB-2002.
XX
PF 25-JUL-2001; 2001WO-US023433.
XX
PR 27-JUL-2000; 2000US-0221478P.
PR 03-AUG-2000; 2000US-0223268P.
PR 21-AUG-2000; 2000US-0227054P.
PR 08-SEP-2000; 2000US-0231121P.
PR 13-SEP-2000; 2000US-0232243P.
PR 15-SEP-2000; 2000US-0232691P.
PR 22-SEP-2000; 2000US-0235146P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
PI Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Wallia NK, Hafalia AJA;
PI Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Graul RC;
PI Warren BA, Lee BA, Ding L;
XX
DR WPI: 2002-188744/24.
DR N-PSDB; AAD29672.
XX
PT New human G-protein coupled receptor polypeptide for diagnosis,
PT prevention and treatment of cell proliferative, neurological,
PT cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
PT disorders.
XX
PS Claim 1; Page 120; 150pp; English.
XX
CC The invention relates to novel human G-protein coupled receptors (GCRC)
CC and their encoding polynucleotides. GCRC is useful as an immunogen for

CC preparing monoclonal and polyclonal antibodies. GCRC is useful for
CC diagnosing, treating and preventing a cell proliferative disorder (e.g.,
CC hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy,
CC Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's
CC disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension,
CC myocardial infarction), gastrointestinal disorder (e.g., gastritis,
CC cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g.,
CC acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma,
CC rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity,
CC osteoporosis), and viral infections. GCRC is useful in a number of drug
CC screening techniques, and to analyse the proteome of a tissue or cell
CC type. GCRC is useful for creating knockin humanised animals or
CC transgenic animals to model human diseases, in somatic or germline gene
CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting differences in the chromosomal location due to translocation,
CC inversion, etc., among normal, carrier or affected individuals, and as
CC hybridization probes for mapping naturally occurring genomic sequences.
CC GCRC is useful in Southern or Northern analysis, dot blot or other
CC membrane-based technologies, in PCR technologies, in dipstick, pin, and
CC microformat enzyme linked immunosorbant (ELISA)-like assays, and in
CC microarrays utilising fluids or tissues from patients to detect altered
CC GCRC expression. The present sequence is human GCRC-6
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 5; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.2e-209;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANSLWSPGSACGLGFVPVYVYLLCLGLPANILTVILSOLVARRQK 60
DB 1 MEHTAHLAANSLWSPGSACGLGFVPVYVYLLCLGLPANILTVILSOLVARRQK 60
QY 61 SSNYLLALAAADILVLFVYVDFLEDFILNMQMPQDPDKLIEVLFSSIHSTWTV 120
DB 61 SSNYLLALAAADILVLFVYVDFLEDFILNMQMPQDPDKLIEVLFSSIHSTWTV 120
QY 121 PLTIDRYAVCHPLKHTVTSYPARTKRVISVYITCFLTSIPYWNPNWTEYISTSVH 180
DB 121 PLTIDRYAVCHPLKHTVTSYPARTKRVISVYITCFLTSIPYWNPNWTEYISTSVH 180
QY 181 HVLIIWHCFVYLVPVCSIPILNSIIVYKLRRKSNFLRGYSTGKTTAILFTITSFATL 240
DB 181 HVLIIWHCFVYLVPVCSIPILNSIIVYKLRRKSNFLRGYSTGKTTAILFTITSFATL 240
QY 241 WAPRIIMILYHLGAPIQNRWLHIMSDIANLALLNTAINPFLYCFISKRFPTMAAATL 300
DB 241 WAPRIIMILYHLGAPIQNRWLHIMSDIANLALLNTAINPFLYCFISKRFPTMAAATL 300
QY 301 KAFFKCKQKQPVQYTNHNSITSSPWSIPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
DB 301 KAFFKCKQKQPVQYTNHNSITSSPWSIPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
QY 361 FEDAIACGVIIIL 372
DB 361 FEDAIACGVIIIL 372

RESULT 3
ABR62521
ID ABR62521 standard; protein; 372 AA.
XX
AC ABR62521;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human G-protein coupled receptor HGPBRMY34.
XX
KW HGPBRMY34; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;
KW human; neuroprotective; nootropic; tranquilizer; antimigraine;
KW neuroleptic; antianemic; antidepressant; anticonvulsant; antiparkinsonian;
KW cytotatic; cardiac; hypotensive; antiangiinal; analgesic; anorectic;
KW anti-HIV; antiasthmatic; osteopathic; uropathic; antitumor; anti-allergic;
KW

gene therapy.
KW
XX Homo sapiens.
XX
XX Key
XX Domain
FT 16..36
FT /label= TM1
FT 65..87
FT /note= "transmembrane domain 1"
FT
FT /label= TM2
FT /note= "transmembrane domain 2"
FT 109..131
FT /label= TM3
FT /note= "transmembrane domain 3"
FT 148..166
FT /label= TM4
FT /note= "transmembrane domain 4"
FT 182..208
FT /label= TM5
FT /note= "transmembrane domain 5"
FT 227..249
FT /label= TM6
FT /note= "transmembrane domain 6"
FT 259..288
FT /label= TM7
FT /note= "transmembrane domain 7"
XX
XX WO2003050256-A2.
XX
XX 19-JUN-2003.
XX
XX 06-DEC-2002; 2002WO-US039290.
XX
XX 06-DEC-2001; 2001US-0338371P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Feder JN, Gopal S, Mintier GA, Ramanathan CS;
XX WPI; 2003-577295/54.
XX N-PSDB; AC050275.
XX
XX New nucleic acid molecule encoding a human G-protein coupled receptor,
XX HGPBRMY34, useful for diagnosing, preventing or treating diseases
XX involving the receptor, for example Parkinson's disease, dementia,
XX asthma, hypertension or cancer.
XX
XX Claim 5; Fig 1A-B; 112pp; English.

XX
XX The present sequence is the protein sequence of human HGPBRMY34, a newly
XX identified G-protein coupled receptor (GPCR) belonging to the group of
XX 'Class A' GPCRs and showing homology to the Pfam model 7 transmembrane
XX receptor, rhodopsin family. HGPBRMY34, also referred to as GPCR-P14
XX and/or GPCR-145, is highly expressed in brain (especially in the
XX amygdala, caudate nucleus, corpus callosum, hippocampus, thalamus,
XX substantia nigra), spinal cord and pituitary, indicating an association
XX in neurological systems and conditions. It is also expressed in the bone
XX marrow and testis. The invention provides HGPBRMY34 polynucleotides,
XX polypeptides and antibodies, expression vectors, host cells and antisense
XX molecules, methods for screening for modulators of HGPBRMY34 activity
XX and/or function, and methods for diagnosing, treating, preventing and
XX screening for disorders and diseases associated with abnormal HGPBRMY34
XX activity, including: a disorder related to aberrant G-protein coupled
XX signalling; a disorder related to aberrant cell cycle regulation;
XX neurological disorders; anxiety; headache; migraine; schizophrenia; manic
XX depression; delirium; dementia; severe mental retardation and
XX dyskinesias, such as Huntington's disease or Gilles de la Tourette's
XX syndrome; Parkinson's disease; brain disorders; spinal cord disorders;
XX affective disorders; neoplastic disorders; cardiovascular disorders;
XX acute heart failure; hypotension; hypertension; angina pectoris;
XX myocardial infarction; an immunological disorder; immune-related
XX disorders; endocrinal diseases; growth disorders; neuropathic pain;
XX obesity; anorexia; HIV infections; cancers; bulimia; asthma; osteoporosis

CC ; psychosis; metabolic disorders; pituitary disorders; urinary retention;
 CC ulcers; allergies; or benign prostatic hypertrophy (all claimed)
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 6; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.2e-209;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEHTHAHLAANSSLSWSPGACGLGFVVPVYYSLLLCGLPANILTVIILSQLVARQK 60
 DB 1 MEHTHAHLAANSSLSWSPGACGLGFVVPVYYSLLLCGLPANILTVIILSQLVARQK 60
 QY 61 SSNNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLBFSSHTSIWTV 120
 DB 61 SSNNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLBFSSHTSIWTV 120
 QY 121 PLTIDRYIAVCHPLKHTVSYSPARTKVIIVSVYITCFLTSIPYYWPNWTDYISTSVH 180
 DB 121 PLTIDRYIAVCHPLKHTVSYSPARTKVIIVSVYITCFLTSIPYYWPNWTDYISTSVH 180
 QY 181 HVLIIHCHFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
 DB 181 HVLIIHCHFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
 QY 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANMLLNTAINFLYCFISKRTWAAATL 300
 DB 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANMLLNTAINFLYCFISKRTWAAATL 300
 QY 301 KAFFKCKQKQVQFYTNHNFSTSSPWSIPANSHCHIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 DB 301 KAFFKCKQKQVQFYTNHNFSTSSPWSIPANSHCHIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
 QY 361 FEDAIACVIL 372
 DB 361 FEDAIACVIL 372

RESULT 4

ADD18023

ID ADD18023 standard; protein; 372 AA.

XX

AC ADD18023;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human G-protein coupled receptor (GPCR) sequence Seq ID19.

XX

KW G protein coupled receptor; GPCR; signal transduction pathway; G protein;
 KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
 KW colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
 KW sleeplessness; hypertension; anxiety; stress; renal failure;
 KW cardiovascular disorder; neural disorder; oncology disorder;
 KW immune disorder; neuroprotective; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 347.351

FT /note= "Encoded by AAGTC"

XX

PN WO2003016478-A2.

XX

PD 27-FEB-2003.

XX

PF 15-AUG-2002; 2002WO-US026017.

XX

PR 20-AUG-2001; 2001US-0313658P.

XX

PR 12-SEP-2001; 2001US-0318675P.

XX

PR 30-OCT-2001; 2001US-0340703P.

XX

PR 26-NOV-2001; 2001US-0333417P.

XX

PR 06-DEC-2001; 2001US-0338367P.

XX

PR 06-FEB-2002; 2002US-0355596P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PA

XX PI Feder JN, Ramanathan CS, Gopal S, Mintier GA;
 XX

XX WPI; 2003-278558/27.

XX N-PSDB; ADD18120.

XX New nucleic acid, useful for manufacturing a medicament for preventing,
 treating or ameliorating a medical condition e.g., neural disorder.
 XX

XX Example 1; SEQ ID NO 19; 251pp; English.

XX This invention relates to novel G protein coupled receptors (GPCRs) and
 their encoding nucleotide sequences. Many medically significant
 biological processes are mediated by proteins participating in signal
 transduction pathways involving G proteins. GPCRs are one of the largest
 receptor superfamilies known. These receptors are biologically important
 and malfunction of these receptors results in diseases such as
 Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal
 pigmentosa and asthma. They are also involved in depression,
 schizophrenia, sleeplessness, hypertension, anxiety, stress, renal
 failure and other cardiovascular, neural, oncology and immune disorders.
 A modulator of the GPCRs of the invention may have neuroprotective
 CC activity whilst the sequences of the invention may be useful for gene
 therapy. The invention may also be useful for manufacturing a medicament
 for preventing, treating or ameliorating a medical condition. The present
 CC sequence is the amino acid sequence of a human GPCR of the invention.

XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 7; Length 372;

Best Local Similarity 100.0%; Pred. No. 1.2e-209; Indels 0; Gaps 0;

Matches 372; Conservative 0; Mismatches 0;

QY 1 MEHTHAHLAANSSLSWSPGACGLGFVVPVYYSLLLCGLPANILTVIILSQLVARQK 60

DB 1 MEHTHAHLAANSSLSWSPGACGLGFVVPVYYSLLLCGLPANILTVIILSQLVARQK 60

QY 61 SSNNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLBFSSHTSIWTV 120

DB 61 SSNNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLBFSSHTSIWTV 120

QY 121 PLTIDRYIAVCHPLKHTVSYSPARTKVIIVSVYITCFLTSIPYYWPNWTDYISTSVH 180

DB 121 PLTIDRYIAVCHPLKHTVSYSPARTKVIIVSVYITCFLTSIPYYWPNWTDYISTSVH 180

QY 181 HVLIIHCHFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240

DB 181 HVLIIHCHFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANMLLNTAINFLYCFISKRTWAAATL 300

DB 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANMLLNTAINFLYCFISKRTWAAATL 300

QY 301 KAFFKCKQKQVQFYTNHNFSTSSPWSIPANSHCHIKMLVYQYDKNGKPIKSRNDSKSSYQ 360

DB 301 KAFFKCKQKQVQFYTNHNFSTSSPWSIPANSHCHIKMLVYQYDKNGKPIKSRNDSKSSYQ 360

QY 361 FEDAIACVIL 372

DB 361 FEDAIACVIL 372

RESULT 5

ADJ87767

ID ADJ87767 standard; protein; 372 AA.

XX

AC ADJ87767;

XX

DT 06-MAY-2004 (first entry)

XX

DE G-coupled protein receptor-related protein #56.

novel protein; G-coupled protein receptor-related protein;
cardiomyopathy; atherosclerosis; cell signal processing-related disorder;
metabolic pathway modulation-related disorder; diabetes; cancer; stroke;
Huntington's disease; epilepsy; anxiety; pain; hypercholesterolaemia;
obesity; hypertension; Crohn's disease; systemic lupus erythematosus;
viral infections; bacterial infection; parasitic infection;
hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;
Alzheimer's disease; tuberosus sclerosis; hypercalcaemia; cerebral palsy.

Unidentified.

WO2002102321-A2.

27-DEC-2002.

18-JUN-2002; 2002WO-US019522.

18-JUN-2001; 2001US-0298994P.

18-JUN-2001; 2001US-0299134P.

04-OCT-2001; 2001US-00972446.

06-JUN-2002; 2002US-00299134.

07-JUN-2002; 2002US-00298994.

(CURA-) CURAGEN CORP.

Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PG;

Pena CEA, Spaderna SK, Zhong M;

WPI; 2003-167441/16.

N-PSDB; ADJ87766.

New MOLX polypeptides and polynucleotides, useful in gene therapy,

particularly for treating or preventing e.g. cardiomyopathy,

atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate

cancer, stroke or pain.

Claim 1; SEQ ID NO 202; 378pp; English.

The invention comprises the amino acid and coding sequences of novel G-

coupled protein receptor-related (MOL) proteins. The DNA and protein

sequences of the invention are useful for treating or preventing a MOL-

associated disorder, such as: cardiomyopathy, atherosclerosis, disorders

associated with cell signal processing and metabolic pathway modulation,

or diabetes. The DNA and protein sequences are also useful for the

treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,

pain, hypercholesterolaemia, obesity, hypertension, Crohn's disease,

systemic lupus erythematosus, viral infections, bacterial infections,

parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau

syndrome, Alzheimer's disease, tuberosus sclerosis, hypercalcaemia, or

cerebral palsy. The present amino acid sequence represents a MOL protein

of the invention.

Sequence 372 AA;

181 HVLIWTHCTVTVLVPCSIFFILNSIIYKLRKSNFRLRGYSTGKTTAILFTTTSIPATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFFLYCFISKRFRMTAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFFLYCFISKRFRMTAAATL 300
QY 301 KAFFKCKQKQVQPYTHNFISITSSPMISPAHSICIKMLVYQYDKNGKPKIKSRNDSKSSYQ 360
DB 301 KAFFKCKQKQVQPYTHNFISITSSPMISPAHSICIKMLVYQYDKNGKPKIKSRNDSKSSYQ 360
QY 361 FEDAIGACVIL 372
DB 361 FEDAIGACVIL 372

RESULT 6

ADI79323

ID ADI79323 standard; protein; 372 AA.

AC ADI79323;

DT 22-APR-2004 (first entry)

DE NOV10a protein sequence, SEQ ID 20.

XX Cytostatic; Immunosuppressive; Antiallergic; Antimicrobial; Vasotropic;
KW Respiratory; Hepatotropic; Virucide; Gastrointestinal; Antidiabetic;
KW Ophthalmological; Antipsoriatic; Neuroprotective; Nootropic;
KW Antiarteriosclerotic; Hypotensive; Cardiant; Cerebroprotective;
KW Gene Therapy; NOVX; human; cancer; myelogenous leukaemia;
KW congenital neonatal autoimmune thrombocytopaenia; immunologic disorder;
KW allergy; infection; asthma; lung disease; reproductive disorder;
KW haemangioma; deafness; liver cirrhosis; hepatitis C; gastric disorder;
KW diabetic retinopathy; psoriasis; multiple sclerosis; atherosclerosis;
KW hypertension; stroke; heart failure; chromosome 1; NOV10a;
KW chemokine receptor.

XX Homo sapiens.

XX WO2004009635-A2.

XX 29-JAN-2004.

XX 04-OCT-2001; 2001WO-US031292.

XX 20-MAR-2001; 2001US-00813432.

XX (CURA-) CURAGEN CORP.

XX Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;

PI Vernet CAM;

XX WPI; 2004-123380/12.

XX N-PSDB; ADI79322.

XX Claim 1; Page 41; 158pp; English.

XX The present invention relates to novel NOVX proteins and their coding
sequences (ADI79304-ADI79327). The sequences are useful for the
manufacture of a medicament for treating a syndrome associated with a
human disease associated with the protein, or for diagnosing and treating
disorders associated with the NOVX protein, such as cancer, myelogenous
leukaemia, congenital neonatal autoimmune thrombocytopaenia,
immunological disorders, allergy and infection, asthma, lung diseases,
reproductive disorders, male and female reproductive diseases,
haemangioma, deafness, liver cirrhosis, hepatitis C, gastric disorders,
diabetic retinopathy, psoriasis, multiple sclerosis, atherosclerosis,
hypertension, stroke and heart failure. NOV10a represents a new member of
the chemokine receptor family and the gene is located on chromosome 1.

XX Sequence 372 AA;

SQ Query Match 100.0%; Score 1967; DB 8; Length 372;

FT /label= TM6
 FT /note= "transmembrane domain 6"
 FT 269. .288
 FT /label= TM7
 FT /note= "transmembrane domain 7"
 PN WO2003050256-A2.
 XX 19-JUN-2003.
 XX 06-DEC-2002; 2002WO-US039290.
 XX 06-DEC-2001; 2001US-0338371P.
 PR (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA Feder JN, Gopal S, Mintier GA, Ramanathan CS;
 PI WPI; 2003-577295/54.
 DR N-PSDB; ACF05276.
 XX
 XX New nucleic acid molecule encoding a human G-protein coupled receptor,
 PT HGRPMY34, useful for diagnosing, preventing or treating diseases
 PT involving the receptor, for example Parkinson's disease, dementia,
 PT asthma, hypertension or cancer.
 XX
 XX Claim 5; Fig 2A-B; 112pp; English.
 XX
 XX The present sequence is the protein sequence of a variant of human
 CC HGRPMY34 (see AB862521) containing a deletion of 3 amino acids but
 CC expected to share at least some of the expression patterns and function
 CC of HGRPMY34. HGRPMY34 is a newly identified G-protein coupled receptor
 CC (GPCR) belonging to the group of 'Class A' GPCRs and showing homology to
 CC the Pfam model 7 transmembrane receptor, rhodopsin family. HGRPMY34 (or
 CC GPCR-P14, GPCR-145) is highly expressed in brain (amygdala, caudate
 CC nucleus, corpus callosum, hippocampus, thalamus, substantia nigra),
 CC spinal cord and pituitary, indicating an association in neurological
 CC systems and conditions. It is also expressed in the bone marrow and
 CC testis. The invention provides HGRPMY34 polynucleotides, polypeptides
 CC and antibodies, expression vectors, host cells and antisense molecules,
 CC methods for screening for modulators of HGRPMY34 activity and/or
 CC function, and methods for diagnosing, treating, preventing and screening
 CC for disorders and diseases associated with abnormal HGRPMY34 activity,
 CC including: a disorder related to aberrant G-protein coupled signalling; a
 CC disorder related to aberrant cell cycle regulation; neurological
 CC disorders; anxiety; headache; migraine; schizophrenia; manic depression;
 CC delirium; dementia; severe mental retardation and dyskinesias such as
 CC Huntington's disease or Gilles de la Tourette's syndrome; Parkinson's
 CC disease; brain disorders; spinal cord disorders; affective disorders;
 CC neoplastic disorders; cardiovascular disorders; acute heart failure;
 CC hypotension; hypertension; angina pectoris; myocardial infarction; an
 CC immunological disorder; immune-related disorders; endocrinal diseases;
 CC growth disorders; neuropathic pain; obesity; anorexia; HIV infections;
 CC cancers; bulimia; asthma; osteoporosis; psychosis; metabolic disorders;
 CC pituitary disorders; urinary retention; ulcers; allergies; or benign
 CC prostatic hypertrophy (all claimed)
 XX
 XX Sequence 369 AA;
 SQ
 Query Match 98.6%; Score 1939.5; DB 6; Length 369;
 Best Local Similarity 99.2%; Pred. No. 1.3e-206;
 Matches 369; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 MEHTHAHLAANSSLSWNSPGSACGLGFPVVPVYVYLLCLGLPANILTVILSOLVARROK 60
 DB 1 MEHTHAHLAANSSLSWNSPGSACGLGFPVVPVYVYLLCLGLPANILTVILSOLVARROK 60
 QY 61 SSNYLLAALAAADILVLFVFDLLEDFILNMQMPQVPDKIIIEVLFSSHTSIWTV 120
 DB 61 SSNYLLAALAAADILVLFVFDLLEDFILNMQMPQVPDKIIIEVLFSSHTSIWTV 120
 QY 121 PLTIDRYIAVCHPLKHTVSVYPARTKRVIVSVITCFLTSIPYVWPNWTEYISTSVH 180

DB 121 PLTIDRYIAVCHPLKHTVSVYPARTKRVIVSVITCFLTSIPYVWPNWTEYISTSVH 180
 QY 181 HVLIIWHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTATLFTTISFATL 240
 DB 181 HVLIIWHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTATLFTTISFATL 240
 QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLLNTAINPFLYCFISKRFRTMAAATL 300
 DB 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLLNTAINPFLYCFISKRFRTMAAATL 300
 QY 301 KAFFKCKQKQVQFYTNHNFSSITSSPWI SPANSHCIKMLVVOYDKNGKPKSRNDSKSSYQ 360
 DB 301 KAFFKCKQKQVQFYTNHNFSSITSSPWI SPANSHCIKMLVVOYDKNGKPKSRNDSKSSYQ 357
 QY 361 FEDAIGACVIL 372
 DB 358 FEDAIGACVIL 369
 RESULT 9
 ADF70485
 ID ADF70485 standard; protein; 591 AA.
 XX
 AC ADF70485;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Orphan receptor ligand-related human protein SeqID108.
 XX
 KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
 KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
 KW GFPuv; Enhanced GFP; EGFP; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003071272-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 21-FEB-2003; 2003WO-JP001901.
 XX
 PR 22-FEB-2002; 2002JP-00045728.
 PR 23-JUL-2002; 2002JP-00213949.
 PR 11-OCT-2002; 2002JP-00298237.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
 XX
 DR WPI; 2003-697654/66.
 DR N-PSDB; ADF70587.
 XX
 PT Transformation of cells with a fusion protein of an orphan receptor
 PT protein with a fluorescent protein useful for identification of ligands
 PT to the orphan receptor.
 XX
 PS Disclosure; SEQ ID NO 108; 594pp; Japanese.
 XX
 CC This invention relates to a novel method of identifying ligands to an
 CC orphan receptor protein which comprises transforming cells with DNA
 CC encoding a fusion protein of the orphan receptor with a fluorescent
 CC protein, so that the fusion protein is expressed in the cells (or cell
 CC membranes isolated from them) and contacting the cells with the potential
 CC ligand to be tested. A suitable fluorescent protein for incorporation in
 CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
 CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
 CC identification of ligands binding to an orphan receptor protein.
 XX
 SQ Sequence 591 AA;
 Query Match 94.8%; Score 1864; DB 7; Length 591;
 Best Local Similarity 96.7%; Pred. No. 6.5e-198;
 Matches 353; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

[illegible]

RESULT 10	
AAU76416	
ID	AAU76416 standard; protein; 353 AA.
XX	
AC	AAU76416;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Novel G-protein coupled receptor TGR8.
XX	
KW	Glycostat; coupled; receptor; cardiovascular; immunomodulator; TGR8;
KW	cytostatic; antiinflammatory; antiulcer; fetal brain;
KW	central nervous system disease; circulatory organ disorder; cancer;
KW	metabolic disease; immunological disease; gastrointestinal disease;
KW	gene therapy; transgenic animal; human.
XX	
OS	Homo sapiens.
XX	
PN	WO200194582-A1.
XX	
PD	13-DEC-2001.
XX	
PF	01-JUN-2001; 2001WO-JP004643.
XX	
PR	02-JUN-2000; 2000JP-00170446.
PR	23-JUN-2000; 2000JP-00194926.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Terao Y, Matsui H, Shintani Y;
XX	
DR	WPI; 2002-164317/21.
DR	N-PSDB; ABK15562, ABK15563.
XX	
PT	Human fetal brain-originated G protein-coupled receptor protein TGR8 and
PT	encoding DNA, for developing drugs to treat e.g. diseases of the central
PT	nervous system or circulatory organs, cancer, and metabolic diseases.
XX	
PS	Claim 1; Fig 2; 102pp; Japanese.
XX	
CC	The invention describes a human fetal brain-originated G protein-coupled
CC	receptor protein, or its salt. The protein and encoded DNA are useful for
CC	developing drugs to treat e.g. diseases of the central nervous system or

circulatory organs, cancer, metabolic diseases, immunological diseases and gastrointestinal diseases. The invention also describes creation of a probe for gene therapy and construction of a transgenic animal. This is the amino acid sequence of the novel G-protein coupled receptor TGR8, described in the method of the invention

Query Match	94.4%	Score 1857;	DB 5;	Length 353;
Best Local Similarity	100.0%;	Pred. No. 1.9e-197;		
Matches 350;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
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Db				
Qy	61	SSNYLLALAAADILVLFVTFVDFLLEDFILNMQMPQPKIEVLFEFSIHSTIVTV	120	
Db				
Qy	61	SSNYLLALAAADILVLFVTFVDFLLEDFILNMQMPQPKIEVLFEFSIHSTIVTV	120	
Db				
Qy	121	PLTIDRYIVACHPLKXHTVSYPARTRKIVSVYITCTLTSIPYTWPNWITVEDYISTSVH	180	
Db				
Qy	121	PLTIDRYIVACHPLKXHTVSYPARTRKIVSVYITCTLTSIPYTWPNWITVEDYISTSVH	180	
Db				
Qy	181	HVLIIWHCFVYLVPCSIPIILANSIIYVKLRKSNFRLRGYSTCKTTAILFTITSIFATL	240	
Db				
Qy	181	HVLIIWHCFVYLVPCSIPIILANSIIYVKLRKSNFRLRGYSTCKTTAILFTITSIFATL	240	
Db				
Qy	241	WAPRIIMILYHLXGAPIQNERLWVHMSDIANMLALLNTAINFFLYCSTIKRFRWMAAATL	300	
Db				
Qy	241	WAPRIIMILYHLXGAPIQNERLWVHMSDIANMLALLNTAINFFLYCSTIKRFRWMAAATL	300	
Db				
Qy	301	KAPFKCQKQPVQPYTNHNFISITSPWTSANSHCIKMLVQYDKNKGPIK	350	
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Db				

RESULT 11	
ABJ04075	
ID	ABJ04075 standard; protein; 353 AA.
XX	
AC	ABJ04075;
XX	
DT	11-OCT-2002 (first entry)
XX	
DE	Human G protein coupled receptor hRUP35.
XX	
KW	Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
KW	hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37.
XX	
OS	Homo sapiens.
XX	
WO	2002042461-A2.
XX	
PN	30-MAY-2002.
PD	
XX	
PF	26-NOV-2001; 2001WO-US044386.
XX	
PR	27-NOV-2000; 2000US-0253404P.
PR	12-DEC-2000; 2000US-0255366P.
PR	20-FEB-2001; 2001US-0270266P.
PR	20-FEB-2001; 2001US-0270286P.
PR	06-APR-2001; 2001US-0282032P.
PR	06-APR-2001; 2001US-0282356P.
PR	06-APR-2001; 2001US-0282358P.
PR	06-APR-2001; 2001US-0282365P.
PR	14-MAY-2001; 2001US-0290917P.
PR	31-JUL-2001; 2001US-0309208P.
XX	
PA	(AREN-) ARENA PHARM INC.
XX	
PI	Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX	

DR WPI: 2002-566565/60.
 XX N-PSDB; ABT04873.
 PT Novel endogenous and non-endogenous versions of G protein-coupled
 PT receptor useful for identification of candidate compounds as receptor
 PT agonists or antagonists for use as therapeutic agents.
 XX
 PS Claim 29; Page 70-72; 84pp; English.
 CC
 CC The present invention provides the protein and coding sequences of
 CC several human G-protein coupled receptors (GPCRs). These can be used in
 CC the identification of candidate compounds as receptor agonists or inverse
 CC agonists having applicability as therapeutic agents. The present sequence
 CC is a GPCR protein of the invention
 XX
 SQ Sequence 353 AA;

Query Match 94.4%; Score 1857; DB 5; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.9e-197;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
 DB 1 MEHTHAHLAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
 QY 61 SSYNLLALAAADILVLFVDFVDFLEDFFILNMQMPQVPDKIEVLEFSSIHSTIVT 120
 DB 61 SSYNLLALAAADILVLFVDFVDFLEDFFILNMQMPQVPDKIEVLEFSSIHSTIVT 120
 QY 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLTSIPYVWPNWTEYISTSVH 180
 DB 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLTSIPYVWPNWTEYISTSVH 180
 QY 181 HVLWIHCHFTVYLVPSCIFPILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
 DB 181 HVLWIHCHFTVYLVPSCIFPILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
 QY 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFPTMAAATL 300
 DB 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFPTMAAATL 300
 QY 301 KAFFKCKQKQVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350
 DB 301 KAFFKCKQKQVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350

RESULT 12

ABB79517
 ID ABB79517 standard; protein; 353 AA.

AC ABB79517;
 XX
 XX 23-SEP-2002 (first entry)
 DT
 XX Human chemokine-like receptor.
 DE
 XX Chemokine-like receptor; G-protein coupled receptor; receptor; human;
 KW HIV infection; cardiovascular disease; asthma;
 KW chronic obstructive pulmonary disease; cardiac;
 KW vasotropic; hypotensive; antiarrhythmic; thrombolytic; anticoagulant;
 KW antiinflammatory; antiallergic; immunomodulator; gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX WO200248358-A2.
 PN
 XX 20-JUN-2002.
 PD
 XX 12-DEC-2001; 2001WO-EP014571.
 PF
 XX 14-DEC-2000; 2000US-0255150P.
 PR 02-APR-2001; 2001US-0280110P.
 PR 21-JUN-2001; 2001US-0299474P.

XX (FARB) BAYER AG.
 XX Smolyar A, Zhu Z, Encinas J, Watanabe S, Okigami H;
 XX WPI: 2002-547858/58.
 DR N-PSDB; ABN84269, ABN84273.
 XX
 PT New isolated polynucleotide encoding a chemokine-like receptor
 PT polypeptide for treating e.g. asthma, myocardial infarction, human
 PT immunodeficiency virus infection, or chronic obstructive pulmonary
 PT disease.
 XX
 XX Claim 25; Fig 2; 114pp; English.

XX The present sequence is the protein sequence of a novel human chemokine-
 CC like receptor of 353 amino acids. The chemokine-like receptor has 7
 CC putative transmembrane domains, consistent with the structure of a G-
 CC protein coupled receptor. Its closest human homologue is C-C chemokine
 CC receptor 3. The novel receptor is expressed at low levels in most
 CC tissues. It is expressed at a high level in phytohaemagglutinin-
 CC stimulated CD8+ cells, but in none of the other immune cells tested. It
 CC may act as a receptor of chemoattractant molecules on activated
 CC lymphocytes and be involved in cell trafficking and homing to sites of
 CC infection, inflammation or tissue injury. Regulation of activity of the
 CC novel receptor can therefore be used to treat cardiovascular,
 CC immunological and inflammatory diseases, including asthma and chronic
 CC obstructive pulmonary disease (COPD). The receptor may also be a target
 CC for viruses that reside in the nervous system. Regulating the binding of
 CC ligands, e.g. chemoattractant molecules or virus particles, to the
 CC receptor can therefore be used to modulate the immune response to inhibit
 CC viral infections, including HIV infection. A claimed method of reducing
 CC activity of an antibody, antisense oligonucleotide or ribozyme) to a
 CC product (preferably RNA or a polypeptide) encoded by a polynucleotide
 CC encoding the human chemokine-like receptor in vivo or in vitro. A claimed
 CC method of treating a chemokine-like receptor dysfunction related disease
 CC selected from HIV infection, a cardiovascular disorder, asthma or COPD
 CC uses a reagent that modulates a function of the receptor
 XX
 SQ Sequence 353 AA;

Query Match 94.4%; Score 1857; DB 5; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.9e-197;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
 DB 1 MEHTHAHLAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
 QY 61 SSYNLLALAAADILVLFVDFVDFLEDFFILNMQMPQVPDKIEVLEFSSIHSTIVT 120
 DB 61 SSYNLLALAAADILVLFVDFVDFLEDFFILNMQMPQVPDKIEVLEFSSIHSTIVT 120
 QY 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLTSIPYVWPNWTEYISTSVH 180
 DB 121 PLTIDRYIAVCHPLKHTVSPARTKRVISVYITCFLTSIPYVWPNWTEYISTSVH 180
 QY 181 HVLWIHCHFTVYLVPSCIFPILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
 DB 181 HVLWIHCHFTVYLVPSCIFPILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
 QY 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFPTMAAATL 300
 DB 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFPTMAAATL 300
 QY 301 KAFFKCKQKQVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350
 DB 301 KAFFKCKQKQVQFYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350

RESULT 13
 ABP98724

DB	61	SSNYLLAALAAADILVLFVDFLEDFILNMOMPOVDPKIIIEVLEFSSIHSTWTV	120
QY	121	PLTIDRYIAVCHPLKYHTVSPARTKRVIVSVYITCFLTSIPYVWPNWINTEDYSTSVH	180
DB	121	PLTIDRYIAVCHPLKYHTVSPARTKRVIVSVYITCFLTSIPYVWPNWINTEDYSTSVH	180
QY	181	HVLWIHCHFTVYLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIPATL	240
DB	181	HVLWIHCHFTVYLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIPATL	240
QY	241	WAPRIIMILYHLYGAPIQNRWLIVHIMSDIANMLALLNTAINFFLYCFISKGFRTMAAATL	300
DB	241	WAPRIIMILYHLYGAPIQNRWLIVHIMSDIANMLALLNTAINFFLYCFISKGFRTMAAATL	300
QY	301	KAPFKCQKOPVQFYTNHNFISITSSPWISPAISHCIKMLVYQYDKNGKPIK	350
DB	301	KAPFKCQKOPVQFYTNHNFISITSSPWISPAISHCIKMLVYQYDKNGKPIK	350
RESULT 14			
ID	ABR44437	standard; protein; 353 AA.	
XX	AC	ABR44437;	
XX	AC	25-JUL-2003 (first entry)	
DT	DT	Human G protein-coupled receptor #SEQ ID 2.	
DE	DE	Human; G protein-coupled receptor; anorectic; eating disorder; obesity.	
XX	KW	Human; G protein-coupled receptor; anorectic; eating disorder; obesity.	
XX	OS	Homo sapiens.	
XX	XX	WO2003027142-A1.	
XX	PD	03-APR-2003.	
XX	PF	19-SEP-2002; 2002WO-JP009626.	
XX	XX	21-SEP-2001; 2001JP-00288278.	
XX	PA	(YAMA) YAMANOUCHI PHARM CO LTD.	
XX	PI	Matsumoto S, Takasaki J, Kurama T, Saito T, Kamohara M, Soga T;	
XX	PI	Hiyama H;	
XX	XX	WPI; 2003-333291/31.	
DR	DR	N-PSDB; ACCT1785.	
XX	XX	New G protein-coupled receptor and encoded gene, useful in screening	
PT	PT	preventives or remedies for eating disorders or obesity.	
XX	PS	Claim 1; Page 34-35; 48pp; Japanese.	
XX	PS	The invention relates to a novel G protein-coupled receptor. The protein	
CC	CC	and its encoded gene are useful for screening preventives or remedies for	
CC	CC	eating disorders or obesity. The current sequence represents a G protein	
CC	CC	coupled receptor sequence	
XX	XX	Sequence 353 AA;	
Query Match			
Best Local Similarity 94.4%; Score 1857; DB 6; Length 353;			
Matches 350; Conservative 100.0%; Pred. No. 1.9e-197;			
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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DB	1	MEHTHAHLAANSLSWSPGSGACGLGFVPPVYVYLLCLGLPANILTVIILSOLVARRQK	60
QY	61	SSNYLLAALAAADILVLFVDFLEDFILNMOMPOVDPKIIIEVLEFSSIHSTWTV	120
DB	61	SSNYLLAALAAADILVLFVDFLEDFILNMOMPOVDPKIIIEVLEFSSIHSTWTV	120

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GenCore version 5.1.6
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Run on: February 12, 2005, 11:09:36 ; Search time 4327 Seconds
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Listing first 45 summaries

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RESULT 1
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DEFINITION Sequence 19 from Patent WO0170978.
ACCESSION AX254975
VERSION AX254975.1 GI:16074503
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Taupier,R.J., Majumder,K., Spaderna,S.K., Smithson,G., Mezes,P.S.
and Vernet,C.A.
TITLE Polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0170978-A 19 27-SEP-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
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ALIGNMENTS

1119 bp DNA linear PAT 10-OCT-2001

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SUMMARIES			
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1	1967	100.0	1119 6 AX254975 Sequence
2	1967	100.0	1130 6 AX375235 Sequence
3	1907	96.9	2117 6 CQ867782 Sequence
4	1903	96.7	1343 6 AX254977 Sequence

Alignment Scores: 1.71e-159 Length: 1119
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Best Local Similarity: 100.00% Mismatches: 0
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DB 61 TCGGCTCGGGCTTGGGTTCTGCGCGGTGTACTACAGCTCTTGTGTGGCTCGGT 120

QY 41 LeuProAlaAsnIleLeuThrValIleLeuSerGlnLeuValAlaAArgGlnLys 60
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QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
DB 361 CGGTAAACCATTTGACAGGTATATCGCTGTCTGCCACCCGCTCAAGTACACAGGTCTCA 420

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DB 421 TACCAGCCCGCACCGGAAGTATTGTAAAGTTTATCATCACCTGCTTCTCGACGACG 480

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QY 181 HisValLeuIleTripletHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
DB 541 CAGCTCCTCATCTGGATCCACTGTCTCACGCTACCTGGTGGTCCCTGTCTCATCTCTTC 600

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QY 221 TyrSerThrGlyThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
DB 661 TACTCCAGGGGAAGACCCGCCATCTTGTTCACCATTTACCTCCATCTTTGCCACACTT 720

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DB 721 TGGGCCCCCGCATCATCATGATTTCTTACCACTCTATGGGGCGCCCATCCAGAACCGC 780

QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuAsnThrAlaIle 280
DB 781 TGGCTGGTACATCATGATCCGACATTTGCCAATGTAGCTTGTGAACACAGCATC 840

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QY 321 IleThrSerSerProTripletSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
DB 961 ATAACAAGTAGCCCTGGATCTCGCGGCAAACTCACACTGCATCAAGATGTGGTGATC 1020

QY 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLeuSerTyrGln 360
DB 1021 CAGTATGACAAAATATGGAAACCTATATAAAGTGTATATGACAGCAAAAGCTCTCCACCC 1080

QY 361 PheGluAspAlaIleGlyValaCysValIleIleLeu 372
DB 1081 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTG 1116

RESULT 2
AX375235 1130 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 25 from Patent WO0210387.
DEFINITION AX375235
ACCESSION AX375235
VERSION AX375235.1 GI:19169953
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thornton,M., Patterson,C., Lal,P., Burford,N., Yue,H., Gandhi,A.R.,
Elliot,V.S., Ramkumar,J., Baughn,M.R., Kallick,D.A., Walla,N.K.,
Hafalia,A.J., Yao,M.G., Lu,Y., Tribouley,C.M., Policky,J.L.,
Kearney,L., Gaul,R.C., Warren,B.A. and Ding,L.
G-Protein coupled receptors
TITLE Patent: WO 0210387-A 25 07-FEB-2002;
JOURNAL Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
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Score: 1967.00 Matches: 372
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Query Match: 100.00% Indels: 0
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US-10-689-832-20 (1-372) x AX375235 (1-1130)

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QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
DB 72 TCGGCTCGGGCTTGGGTTCTGCGCGGTGTACTACAGCTCTTGTGTGGCTCGGT 131

QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAArgGlnLys 60
DB 132 TTACAGCAATATCTTGCAGTGTATCTCTCCAGCTGGTGGCAGAGACAGAG 191

QY 61 SerSerTyrAsnTyrLeuLeuAlaAlaAAspIleLeuValLeuPhePheIle 80
DB 192 TCTCTCAACTATCTCTTGGCACTCGCTGTGCGCATCTTGGTCTCTTTTTCATA 251

QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
DB 252 GTGTTTGGGACTTCTCTGTGGAGATTTCATCTTGAACATGCAGATGCCCTCAGGTCCCG 311

QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTripletThrVal 120
DB 312 GACAGATCATAGAGTGTGGAAATCTCATTCATCCACCTCCATATGATGATCTGTA 371

QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
DB 372 CGGTTAACCATTTGACAGGTATATCGCTGTGCGCAACCCGCTCAAGTACACAGGTCTCA 431

QY 141 TyrProAlaAaThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
 Db TACCAGCCGACCCGAAAGTCATTGTGAAGTGTATTTACATCACTGCTTCTGACCAAGC 491
 QY 161 IleProTyrTyrTyrTyrProAsnIleTyrThrGluAspTyrIleSerThrSerValHis 180
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 QY 181 HisValLeuIleTyrPheHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
 Db CACGTCCTCATCTGCATCCACTGCTTACCGCTTACCTGTGGTGGCCCTGCTCCATCTTCTTC 611
 QY 201 IleLeuAsnSerIleIleValTyrIleValLysLeuArgLysSerAsnPheArgLeuArgGly 220
 Db ATCTTGAACTCAATCTTGTGTACAGCTCAGGAGGAGCAATTTTGTCTCCGTCGC 671
 QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
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 QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
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 QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
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 QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
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 QY 321 IleThrSerSerProTyrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
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 QY 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerSerTyrGln 360
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RESULT 3

LOCUS CQ867782 2117 bp DNA linear PAT 13-SRP-2004
 DEFINITION Sequence 1 from Patent WO2004074841.
 ACCESSION CQ867782

VERSION CQ867782.1 GI:51997901

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Murphy, A. J. and Croll-Kalish, S.

AUTHORS

activity

TITLE

Kor3l-like proteins and methods of modulating kor3l-mediated

JOURNAL

Patent: WO 2004074841-A 1 02-SEP-2004;

REGENERON PHARMACEUTICALS, INC. (US); Murphy, Andrew J. (US);

Croll-Kalish, Susan (US)

FEATURES

source

1. .2117

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

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 Percent Similarity: 83.22% Mismatches: 0
 Best Local Similarity: 96.95% Indels: 75
 Query Match: 6 Gaps: 1
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 Db 340 TCGGCTCGCGCTTGGGTTTGGTGGCGGTGCTACTACAGCTCTTGTGTGCTCGGT 399
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 QY 161 IleProTyrTyrTyrTyrProAsnIleTyrThrGluAspTyrIleSerThrSerValHis 180
 Db 760 ATCCCTATTACTTGGTGGCCCAACATCTGAGCTGAAGACTACATCAGACCTCTGTGCAT 819
 QY 181 HisValLeuIleTyrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
 Db 820 CACGTCTCATCTGGATCCACTGCTTACCGCTTACCTGGTGGCTGCTTCTTCTTCTTC 879
 QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220
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 QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
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Qy 341 GlnTyrAspLysAasnGlyLysProIle-Lys----- 350

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RESULT 4

AX254977 AX254977 1343 bp DNA linear PAT 10-OCT-2001

LOCUS AX254977 Sequence 21 from Patent WO0170978.

DEFINITION AX254977

ACCESSION AX254977.1 GI:16074504

VERSION

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Taupier, R. J., Majumder, K., Spaderna, S. K., Smithson, G., Mezes, P. S.

TITLE and Vernet, C. A.

JOURNAL Polypeptides and nucleic acids encoding same

Curagen Corporation (US)

FEATURES Location/Qualifiers

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

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Pred. No.: 6,61e-154 Length: 1343

Score: 1903.00 Matches: 371

Percent Similarity: 83.00% Conservative: 0

Best Local Similarity: 83.00% Mismatches: 1

Query Match: 96.75% Indels: 75

DB: 6 Gaps: 1

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Db 422 TACCAGCCCGACCCCGAAGTCACTTGAAGTGTTHACATCACTGCTTCTGACACAGC 481

Qy 161 IleProTyrTrrpTrrpProAsnIleTrrpThrGluAspTrrpIleSerThrSerValHis 180

Db 482 ATCCCTTATTACTTGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 541

Qy 181 HisValLeuIleTrrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200

Db 542 CACGCTCTCATCTGGATCCACTGCTTACCGCTTACCTGGTGGTGGTGGTGGTGGTGGT 601

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Qy 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240

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Qy 350 ----- 350


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RESULT 6
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LOCUS   AX463227
DEFINITION Sequence 1 from Patent WO0248358.
ACCESSION AX463227
VERSION   AX463227.1 GI:21886199
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Smolyar,A., Zhu,Z., Encinas,J., Watanabe,S. and Okigami,H.
TITLE     Regulation of human chemokine-like receptor
JOURNAL   Patent: WO 0248358-A 1 20-JUN-2002;
          Bayer Aktiengesellschaft (DE)
FEATURES
          Location/Qualifiers
            source
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Score:          1857.00        Matches:      350
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Best Local Similarity: 100.00% Mismatches: 0
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RESULT 7
BD183203
LOCUS   BD183203
DEFINITION Novel G protein-coupled receptor and its DNA.
ACCESSION BD183203
VERSION   BD183203.1 GI:31875403
KEYWORDS JP 2002345481-A/3.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1062)
AUTHORS   Terao,Y., Mateui,H. and Shintani,Y.
TITLE     Novel G protein-coupled receptor and its DNA
JOURNAL   Patent: JP 2002345481-A 3 03-DEC-2002;
          TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT   OS Homo sapiens (human)
          PN JP 2002345481-A/3
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          PF 01-JUN-2001 JP 2001166688
          PI YASUKO TERAO, HIDEKI MATSUI, YASUSHI SHINTANI
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Score:		Conservative: 0
Percent Similarity:		100.00% Mismatches: 0
Best Local Similarity:		Indels: 0
Query Match:		94.41% Gaps: 0
Db:		6
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Db	1 ATGGAGCACAAGCAGCCCACTCGCAGCCCAACAGCTCGCTGCTTGGTGGTCCCCGGC	60
Qy	21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly	40
Db	61 TCGGCTCGGCTTGGGTTTCGTGCCGTGGTCTACTACAGCTCTTGTGCTCGCTCGT	120
Qy	41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAlaArgGlnLys	60
Db	121 TTACAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAAG	180
Qy	61 SerSerTyrAsnTyrLeuLeuAlaAlaAspIleLeuValLeuPhePheIle	80
Db	181 TCCTCTACAACTATCTCTGGCACTCGCTGCTGCCGACATCTTGGTCTCTTTTTCATA	240
Qy	81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro	100
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Db	421 TACCCAGCCCGCACCGGAAAGTCATTGTAAGTGTTCATCACCTGCTTCTCGACACG	480
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Db	481 ATCCCTATTACTGGTGGCCCAACATCTGGAATGGAAGATCATCATCAGCACCTCTGTGCAT	540
Qy	181 HisValLeuIleTyrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe	200
Db	541 CACGTCCTCATCTGGATCCACTGCTTACCGTACTACCTGGTGGCTGCTCCATCTTCTTC	600
Qy	201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly	220
Db	601 ATCTTGAATCAATCATTTGTGTACAGCTCAGGAGGAAGACAAATTTTCTGCTCGGTGC	660
Qy	221 TyrSerThrGlySerThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu	240
Db	661 TACTCCACGGGAGACCAACCGCATCTTGTTCACCATTACCTCCATCTTGGCACATT	720
Qy	241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg	260
Db	721 TGGGCCCCCGCATCATCATGATTTTACCACTCTATGGGGCGCCCATCCAGAACCGC	780
Qy	261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuAsnThrAlaIle	280
Db	781 TGGCTGGTGACATCATGATGCCACATGTCACATGCTAGCCCTTCTGAAACACAGCCATC	840
Qy	281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaAlaThrLeu	300
Db	841 NAATCTTCTCTACTGCTTTCATCAGCAGCGGTTCCGACCATGGCAGCCCGCAGCTC	900
Qy	301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer	320
Db	901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTACACCAATCATTAACCTTTC	960
Qy	321 IleThrSerSerProTyrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr	340
Db	961 ATAACAAGTAGCCCTTGGATCTCGCGGCAAACTCACATGTCATCAAGATGTGGTGATC	1020
Qy	341 GlnTyrAspLysAsnGlyLysProIleLys 350	
Db	1021 CAGTATGACAAAATGGAAAACCTATATAA 1050	
RESULT 9		
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DEFINITION		Sequence 15 from Patent WO0242461.
ACCESSION		AX498192
VERSION		AX498192.1 GI:23343117
KEYWORDS		synthetic construct
SOURCE		synthetic construct
ORGANISM		other sequences; artificial sequences.
REFERENCE		1
AUTHORS		Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.
TITLE		Endogenous and non-endogenous versions of human g protein-coupled receptors
JOURNAL		Patent: WO 0242461-A 15 30-MAY-2002; Arena Pharmaceuticals, Inc. (US)

Qy 281 AsnPheLeuTyrCysPheIleSerIleArgPheArgThrMetAlaAlaThrLeu 300
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RESULT 10

BD103851 1062 bp DNA linear PAT 27-AUG-2002
 LOCUS Novel G protein-coupled receptor and its DNA.

DEFINITION Novel G protein-coupled receptor and its DNA.
 ACCESSION BD103851
 VERSION BD103851.1 GI:22649425
 KEYWORDS WO 0194582-A/3.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1062)
 Terao, Y., Matsui, H. and Shintani, Y.
 Novel G protein-coupled receptor and its DNA
 Patent: WO 0194582-A 3 13-DEC-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUKO TERAO, HIDEKI MATSUI, YASUSHI SHINTANI

AUTHORS

OS Homo sapiens (human)
 PN WO 0194582-A/3
 PD 13-DEC-2001

TITLE

PR 01-JUN-2001 WO 2001JP004643
 PR 02-JUN-2000 JP OP 170446, 23-JUN-2000 JP OP 194926 PI
 YASUKO TERAO, HIDEKI MATSUI, YASUSHI SHINTANI

JOURNAL

PC C12N15/12, C12P21/02, C07K14/705, C07K16/28, A61K45/00, A61P25/00,
 PC A61P29/00,
 PC A61P9/00, A61P35/00, A61P3/00, A61P1/00, G01N33/566, PC
 G01N33/50,
 PC G01N33/15

CC

CC Novel G protein-coupled receptor and its DNA

FH

FH Key Location/Qualifiers

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FT source 1..1062

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Location/Qualifiers
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.41% Indels: 0
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 Qy 21 SerAlaCysGlyLeuGlyPheValProValTyrTrpSerLeuLeuCysLeuGly 40
 Db 61 TCGGCTCGCGCTGGGTTCGTGGCGGCTGCTTACTACAGCCTCTTGTGTCGCTCGGT 120

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 Qy 61 SerSerTyrAenTyrIleLeuAlaLeuAlaAaAspIleLeuValLeuPhePheIle 80
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 Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAenMetGlnMetProGlnValPro 100
 Db 241 GTGTTTGTGGACTTCTCTGTGGAGATTTCATCTTGAACATGAGATGCTCTAGTCCCC 300
 Qy 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
 Db 301 GACAAGATCATAGAAGTGTGGAAATCTCATCCATCCACACCTCCATATGGATTACTGTA 360
 Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
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 Db 661 TACTCCACGGGGAAGACCCAGCCCATCTTGTTCACCATTTACCTCCATCTTTGGCACACTT 720
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RESULT 11

BD103852 1062 bp DNA linear PAT 27-AUG-2002
 LOCUS Novel G protein-coupled receptor and its DNA.
 DEFINITION Novel G protein-coupled receptor and its DNA.
 ACCESSION BD103852
 VERSION BD103852.1 GI:22649426
 KEYWORDS WO 0194582-A/4.
 SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1062)
JOURNAL Terso,Y., Matsui,H. and Shintani,Y.
Novel G protein-coupled receptor and its DNA
Patent: WO 0194582-A 4 13-DEC-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,YASUKO TERA0,HIDEKI MATSUI, YASUSHI
SHINTANI
COMMENT OS Homo sapiens (human)
PV WO 0194582-A/4
PD 13-DEC-2001
PF 01-JUN-2001 WO 2001JP004643
PR 02-JUN-2000 JP OP 170446,23-JUN-2000 JP OP 194926 PI
YASUKO TERA0,HIDEKI MATSUI,YASUSHI SHINTANI
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PC A61P29/00,
PC A61P9/00,A61P35/00,A61P3/00,A61P37/00,A61P1/00,G01N33/566, PC
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PC G01N33/15
CC Novel G protein-coupled receptor and its DNA
FH Key Location/Qualifiers
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Pred. No.: 4,44e-150 Length: 1062
Score: 1857.00 Matches: 350
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.41% Indels: 0
DB: 6 Gaps: 0
US-10-689-832-20 (1-372) x BD103852 (1-1062)
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Db 1 ATGGAGCACAGCAGCCACCTCGCAGCCACAGCTCGCTGCTGTGGTGGTCCCGGC 60
QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrSerLeuLeuLeuCysLeuGly 40
Db 61 TCGGCCTCGCGGTGGGTTTCGGTCCCGTGGTCTACTACAGCCTCTTGTGCTCGGT 120
QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAlaArgGlnLys 60
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Db 181 TCTCTCTACACTATCTCTGGCACTCGCTGCTGGCGACATCTTGGTCTCTTTTCATA 240
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QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
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AY635179 1167 bp mRNA linear PRI 04-JUL-2004
LOCUS Homo sapiens G protein-coupled receptor 139 (GPR139) mRNA, complete
DEFINITION cds:
ACCESSION AY635179
VERSION AY635179.1 GI:49413551
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1167)
AUTHORS Bonner,T.I., Nagle,J.W. and Kauffman,D.
TITLE Complete coding sequence of GPR139
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1167)
AUTHORS Bonner,T.I., Nagle,J.W. and Kauffman,D.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2004) Lab of Genetics, NIMH, Bldg 36, Rm 3D06,
MSC4094, Bethesda, MD 20892-4094, USA
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RESULT 14
AX463235 LOCUS AX463235 1062 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 9 from Patent WO0248358.
ACCESSION AX463235
VERSION AX463235.1 GI:21886203
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Smolyar, A., Zhu, Z., Encinas, J., Watanabe, S. and Okigami, H.
AUTHORS Regulation of human chemokine-like receptor
TITLE Patent: WO 0248358-A 9 20-JUN-2002;
JOURNAL Bayer Aktiengesellschaft (DE)
FEATURES
Location/Qualifiers
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source 1..1062
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
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Percent Similarity: 90.74% Conservative: 1
Best Local Similarity: 90.46% Mismatches: 0
Query Match: 88.05% Indels: 34
DB: 6 Gaps: 2
US-10-689-832-20 (1-372) x AX463235 (1-1062)

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QY 184 IleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePheIleLeuAsn 203
Db 550 ATCTGGATCCCATGCTTACCGCTGTACCTGTGGTGGCCCTGCTCCATCTTCTTCACTTGAAC 609
QY 204 SerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGlyTyrSerThr 223
Db 610 TCAATCATTTGTACAACTCAGGAGGAGAGCAATTTTCTCGTCTCGTGGCTACTCCAGC 669
QY 224 GlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeuTrpAlaPro 243
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QY 244 ArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArgTrpLeuVal 263
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QY 264 HisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIleAsnPhePhe 283
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Db 850 CTCTACTGCTTCATCAGCAGCGGTCGACACATGCGACCGCCAGCTCAGGCTTTC 909
Qy 304 PheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSerIleThrSer 323
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Qy 324 SerProTyrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyrGlnTyrAsp 343
Db 970 AGCCCTTGGATCTCGCGGCAAACTCACCTGCATCAAGATGCTGGTGTACCAAGTATGAC 1029
Qy 344 LysAsnGlyLysProIleLys 350
Db 1030 AAAATGGAAACCTATANA 1050

RESULT 15
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DEFINITION Sequence 6 from Patent WO0248358.
ACCESSION AX463232
VERSION AX463232.1 GI:21886202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Smolyar,A., Zhu,Z., Encinas,J., Watanabe,S. and Okigami,H.
TITLE Regulation of human chemokine-like receptor
JOURNAL Patent: WO 0248358-A 6 20-JUN-2002;
Bayer Aktiengesellschaft (DE)
FEATURES
source
1..1826
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:
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Score: 1673.00 Matches: 330
Percent Similarity: 81.48% Conservative: 0
Best Local Similarity: 81.48% Mismatches: 0
Query Match: 85.05% Indels: 75
DB: 6 Gaps: 1

US-10-689-832-20 (1-372) x AX463232 (1-1826)
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Qy 63 TyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPheIleValPhe 82
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Qy 83 ValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValProAspLys 102
Db 290 GTGGACTTCTGTTGGAAGATTTTCATCTTGAACATGCAGATGCTCAGGTCCCGCAAG 349
Qy 103 IleIleGluValLeuGluPheSerSerIleHisThrSerIleThrPheValProLeu 122
Db 350 ATCATAGAGTGTGGAAATTTCTCATCCATCCACACCTCCATATGGATTAAGTACCGTTA 409
Qy 123 ThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSerTyrPro 142
Db 410 ACCATAGACAGGTATATCGCTGCTGCCACCGCTCAAGTACCACACAGGCTCATACCCA 469
Qy 143 AlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSerIlePro 162
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Search completed: February 12, 2005, 15:01:48
Job time : 4341 secs

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Qy 183 LeuIleTyrPheIleHisCysPheThrValTyrLeuValProCysSerIlePheIleLeu 202
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Db 710 ACGGGAGACACACCGCATCTTGTTCACCATTTACCTCTTTCGCCACACTTGGGCC 769
Qy 243 ProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArgTyrLeu 262
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Qy 343 AspLysAsnGlyLysProIle-Lys----- 350
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Qy 350 ----- 350
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Db 1310 TCCACAGACTCGTAATGACAGCAAAAGCTCTTACCAAGTTTGAAGATGCCATTGGAGCTTG 1369
Qy 368 sValIleIleLeu 372
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 12, 2005, 10:59:01 ; Search time 560 Seconds
(without alignments)
3932.400 Million cell updates/sec

Title: US-10-689-832-20

Perfect score: 1967

Sequence: 1 MEHTHAHLAANSLSWSPG.....NDSKSSYQFIDAIGACVIL 372

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
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13: Geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1967	100.0	1119	4 AAS15730	Aas15730 DNA encod
2	1967	100.0	1119	10 ADJ87766	Adj87766 G-coupled
3	1967	100.0	1119	12 ADI79322	Adi79322 NOV10a co
4	1967	100.0	1119	12 ADO56001	Ado56001 DNA encod
5	1967	100.0	1130	6 AAD29672	Aad29672 Human G-p

6	1967	100.0	2198	9 ACF05275	Acf05275 Human G-p
7	1939.5	98.6	1110	9 ACF05276	Acf05276 Human G-p
8	1939.5	98.6	2189	10 ADD18120	Add18120 Human G-p
9	1907	96.9	2117	13 ADR16433	Adr16433 Human KOR
10	1903	96.7	1343	4 AAS15731	Aas15731 DNA encod
11	1903	96.7	1343	10 ADJ87768	Adj87768 G-coupled
12	1903	96.7	1343	12 ADI79324	Adi79324 NOV11 cod
13	1903	96.7	1343	12 ADO56003	Ado56003 DNA encod
14	1903	96.7	2273	12 ADO28955	Ado28955 Human nov
15	1879	95.5	1526	6 AAD46858	Aad46858 Human 7TM
16	1879	95.5	1526	8 ACA60889	Ac60889 Human cdn
17	1879	95.5	1526	10 ABS57024	Ab57024 cdNA enco
18	1864	94.8	1776	10 ADP70587	Adp70587 Orphan re
19	1857	94.4	1059	6 ABN84269	Abn84269 Human che
20	1857	94.4	1062	6 ABK15562	Abk15562 cdNA enco
21	1857	94.4	1062	6 ABK15563	Abk15563 cdNA enco
22	1857	94.4	1062	6 ABT04873	Abt04873 Human G p
23	1857	94.4	1062	10 ACC44115	Acc44115 Human AXO
24	1857	94.4	1062	10 ACC71785	Acc71785 Human G P
25	1857	94.4	1202	8 ABV73364	Abv73364 Human TGR
26	1741	88.5	1038	8 ABV73373	Abv73373 Mouse TGR
27	1741	88.5	1038	12 ADO28957	Ado28957 Mouse nov
28	1732	88.1	1062	6 ABN84273	Abn84273 Human che
29	1673	85.1	1826	6 ABN84272	Abn84272 Human che
30	1628	82.8	957	12 ADI79347	Adi79347 NOV10b co
31	1628	82.8	957	12 ADO56026	Ado56026 DNA encod
32	1623	82.5	1002	6 AAD27501	Aad27501 Human G-p
33	1623	82.5	1002	10 AAD61658	Aad61658 Human GPC
34	1623	82.5	1032	6 ABN84271	Abn84271 Human che
35	1623	82.5	1070	6 ABN84270	Abn84270 Human che
36	1623	82.5	1158	6 ABZ42880	Abz42880 Human GPC
37	1623	82.5	1167	13 ADQ89945	Adq89945 Antagonia
38	1616	82.2	1000	6 AAD28102	Aad28102 Human thy
39	1607	81.7	946	10 ADJ87879	Adj87879 G-coupled
40	1471	74.8	864	4 AAS42811	Aas42811 Human G p
41	1447	73.6	867	6 AAS98134	Aas98134 Human DNA
42	1447	73.6	894	6 AAS98143	Aas98143 Human DNA
43	1421	72.2	963	10 ADC12695	Adc12695 Human GPC
44	1317	67.0	795	6 AAS98071	Aas98071 Human DNA
45	1317	67.0	795	8 ABZ42552	Abz42552 Human G p

ALIGNMENTS

RESULT 1
AAS15730
ID AAS15730 standard; cdNA; 1119 BP.

XX AAS15730;

XX 14-FEB-2002 (first entry)

XX DNA encoding chemokine receptor family related protein, NOV10.

XX NOV; cytostatic; psoriasis; neutropenic; neuroprotectant;
XX cerebroprotective; hepatic; anti-inflammatory; diabetes; anaemia;
XX haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;
XX differentiation; proliferation; haematopoiesis; wound healing;
XX angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;
XX haemophilia; allergy; Pender syndrome; skeletal dysplasia;
XX ischaemic injury; neuroepithelial disorder; hepatitis; heart failure;
XX chemokine receptor; chromosome 1; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 1..1119
XX /tag= a
XX /product= "Chemokine receptor related protein, NOV10"
XX sig_peptide 1..141
XX mat_peptide 142..1116
XX /tag= b
XX /tag= c

/note= "Mature chemokine receptor related protein, NOV10"

WO200170978-A2.

27-SEP-2001.

20-MAR-2001; 2001WO-US009093.

20-MAR-2000; 2000US-0190768P.

20-MAR-2000; 2000US-0190835P.

22-MAR-2000; 2000US-0190972P.

22-MAR-2000; 2000US-0191199P.
24-MAR-2000: 2000US-0191947P.

28-MAR-2000; 2000US-0192657P.

28-MAR-2000; 2000US-0192664P.

28-MAR-2000; 2000US-0192665P.
29-MAR-2000; 2000US-0192984P

28-MAR-2000; 2000US-0192984P.
29-MAR-2000; 2000US-0192836P.

31-MAR-2000; 2000US-0193843P.

11-11-11

(CURA-) CURAGEN CORP.

Taupier RJ, Majumder

vernet CAM;

WPI; 2001-6

P-PSDB; AAU10067.

100

Polypeptides and nucleic acids related to chloride channel, insulin-like growth factor family of proteins, useful for diagnosing and treating cancer, cystic fibrosis, acute pancreatitis and Alzheimer' disease.

Claim 9; Page 42; 151pp; English.

The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX polypeptides are useful for treating pathology associated with NOVX polypeptide, determining the presence of or predisposition to a disease associated with altered levels of NOVX, identifying agents binding to NOVX and treatment of disorders associated with altered expression of members of chloride channel-associated proteins e.g. cystic fibrosis and congenital myotonia. NOVX proteins are useful in treatment of disorders, including psoriasis, cancer, diabetes, metabolic disorders of pancreas, e.g. acute pancreatitis, abnormal growth and accumulation of mast cells in one or more organs (e.g. haemophilia, anaemia). Pendred syndrome, skeletal dysplasias, disorders characterised by altered cell shape, motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the treatment of disorders of vascular smooth muscle cell differentiation, (e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are useful to screen for molecules which inhibit or enhance NOVX activity or function and are useful as targets for the identifying small molecules, that modulate or inhibit e.g. neurogenesis, proliferation, motility, cell differentiation, haematopoiesis, wound healing and angiogenesis. NOV sequences are also useful for: identifying a cell or tissue type in a biological sample; amplifying DNA sequences from very small biological samples e.g. hair or skin or body fluids and as primers and probes to identify and/or clone NOVX homologues. NOVX proteins are useful immunogens to generate antibodies to monitor protein levels and modulate NOVX activity. Cells comprising the nucleic acids are useful for producing transgenic animals, for studying the function and/or activity of NOVX protein and identifying and/or evaluating modulators of NOVX protein activity. This sequence encodes NOV10 (located on chromosome 1) related to the chemokine receptor family of proteins, one of 12 NOV polypeptides described in the method of the invention.

Sequence 1119 BP; 258 A; 353 C; 220 G; 288 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,528-187	Length:	1119
Score:	1967.00	Matches:	372
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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Qy 361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
Db 1081 TTTGAAGATGCCATTGGAGCTTGTGTCATCATCTG 1116

RESULT 2

ADJ87766
ID ADJ87766 standard; DNA; 1119 BP.

XX AC ADJ87766;

DT 06-MAY-2004 (first entry)

DE G-coupled protein receptor-related protein coding sequence #56.

XX novel protein; G-coupled protein receptor-related protein;
KW cardiomyopathy; atherosclerosis; cell signal processing-related disorder;
KW metabolic pathway modulation-related disorder; diabetes; cancer; stroke;
KW Huntington's disease; epilepsy; anxiety; pain; hypercholesterolaemia;
KW obesity; hypertension; Crohn's disease; systemic lupus erythematosus;
KW viral infections; bacterial infection; parasitic infection;
KW hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;
KW Alzheimer's disease; tuberosclerosis; hypercalcaemia; cerebral palsy;
KW gene; ds.

XX Unidentified.

XX WO2002102321-A2.

XX 27-DEC-2002.

XX 18-JUN-2002; 2002WO-US019522.

XX 18-JUN-2001; 2001US-0298994P.

XX 04-OCT-2001; 2001US-0299134P.

XX 06-JUN-2002; 2002US-00972446.

XX 07-JUN-2002; 2002US-00299134.

XX (CURA-) CURAGEN CORP.

XX Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS;

XX Pena CE, Spaderma SK, Zhong M;

XX WPI: 2003-167441/16.

XX P-PSDB; ADJ87767.

XX New MOLX polypeptides and polynucleotides, useful in gene therapy,

XX particularly for treating or preventing e.g. cardiomyopathy,

XX atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate

XX cancer, stroke or pain.

XX Claim 8; SEQ ID NO 201; 378pp; English.

XX The invention comprises the amino acid and coding sequences of novel G-
coupled protein receptor-related (MOL) proteins. The DNA and protein
sequences of the invention are useful for treating or preventing a MOL-
associated disorder, such as: cardiomyopathy, atherosclerosis, disorders
associated with cell signal processing and metabolic pathway modulation,
or diabetes. The DNA and protein sequences are also useful for the
treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,
pain, hypercholesterolaemia, obesity, hypertension, Crohn's disease,
systemic lupus erythematosus, viral infections, bacterial infections,
parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau
syndrome, Alzheimer's disease, tuberosclerosis, hypercalcaemia, or
cerebral palsy. The present DNA sequence encodes a MOL protein of the
invention.

XX Sequence 1119 BP; 258 A; 353 C; 220 G; 288 T; 0 U; 0 Other;

SQ Alignment Scores:

Pred. No.:	2.52e-187	Length:	1119
Score:	1967.00	Matches:	372
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
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Qy	21	SerAlaCysGlyLeuGlyPheValProValValTyrSerLeuLeuLeuCysLeuGly	40
Db	61	TGGCGCTGCGGCTTGGGTTTCGTGCGGTGCTACTACAGCCTCTTGTGTGCTCGGT	120
Qy	41	LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaArgGlnLys	60
Db	121	TTACCCAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAG	180
Qy	61	SerSerTyrAsnTyrLeuLeuAlaAlaAlaAspIleLeuValLeuPheIle	80
Db	181	TCTCTCTACACTATCTCTTGGCACTCGCTGCTGCGCAGCATCTTGGTCTCTTTTCATA	240
Qy	81	ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro	100
Db	241	GTGTTTGTGGACTTCTCTGTGGAGATTTTCATCTTGAACATGCAGATGCTCAGGTCCCC	300
Qy	101	AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal	120
Db	301	GACAGATCATAGAAGTGTGGAATTTCTCATCATCCACACCTCCATATGGATTACTGTA	360
Qy	121	ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer	140
Db	361	CGTTTAACCTTGACAGGTAATTCGCTGCTGCCACCCGCTCAAGTACACACGGTCTCA	420
Qy	141	TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer	160
Db	421	TACCCAGCCCGCACCGGAAAGTCATTGTAAGTGTGTTTACATCACCTGCTTCTGACACGC	480
Qy	161	IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis	180
Db	481	ATCCCCATATTACTGTGGGCCCAACATCTGSACTGGAAGACTATCATCAGCAGCTCTGTCAT	540
Qy	181	HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe	200
Db	541	CACGTCCTCATCTGGATCCACTGCTTACCGTCTACCTGTGCGCTGCTTCTTCTTCTTC	600
Qy	201	IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly	220
Db	601	ATCTTGAACCTCAATCATCTGTTGTAAGCTCAGGAGGAGAGCAATTTTCTCTCCGTGGC	660
Qy	221	TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu	240
Db	661	TACTCCACGCGGAGACACCGCCCATCTTGTTCACCATTACCTTCCATCTTTGACACATT	720
Qy	241	TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyValaProIleGlnAsnArg	260
Db	721	TGGGCCCCCGCATCATCATGATTTTATACCACTCTATGGGGCGGCCCATCCAGAACCCG	780
Qy	261	TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle	280
Db	781	TGGTGTGTACACATCATGTCCGACATTCGCAACATGCTAGCCCTTCTGACACAGCCATC	840
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 QY 341 GlnTyrAspLysGlyLysProLeuSerArgAsnAspSerLysSerSerTyrGln 360
 Db |||||
 QY 361 PheGluAspAlaIleGlyAlaCysValIleLeu 372
 Db |||||
 QY 1081 TTGAAGATGCCATTGGAGCTTGTGTCATCATCTG 1116

RESULT 3

ADI79322

ID ADI79322 standard; DNA; 1119 BP.

XX

AC ADI79322;

XX

DT 22-APR-2004 (first entry)

XX

DE NOV10a coding sequence, SEQ ID 19.

XX

KW Cytostatic; Immunosuppressive; Antiallergic; Antimicrobial; Vasotropic;
 KW Respiratory; Hepatotropic; Virucide; Gastrointestinal; Antidiabetic;
 KW Ophthalmologic; Antipsoriatic; Neuroprotective; Nootropic;
 KW Antiartherosclerotic; Hypotensive; Cardiant; Cerebroprotective;
 KW Gene Therapy; NOV; human; cancer; myelogenous leukemia;
 KW congenital neonatal autoimmune thrombocytopaenia; immunological disorder;
 KW allergy; infection; asthma; lung disease; reproductive disorder;
 KW haemangioma; deafness; liver cirrhosis; hepatitis C; gastric disorder;
 KW diabetic retinopathy; psoriasis; multiple sclerosis; atherosclerosis;
 KW hypertension; stroke; heart failure; chromosome 1; NOV10a;
 KW chemokine receptor; gene; db.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

FT 1..1119

FT /*tag= a

FT /product= "NOV10a"

XX

PN WO2004009635-A2.

XX

XX 29-JAN-2004.

XX

PF 04-OCT-2001; 2001WO-US031292.

XX

PR 20-MAR-2001; 2001US-00813432.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;

PI Vernet CAM;

XX

DR WPI; 2004-123380/12.

XX

XX P-PSDB; ADI79323.

XX

XX Claim 8; Page 41; 158pp; English.

XX

CC The present invention relates to novel NOVX proteins and their coding
 CC sequences (ADI79304-ADI79327). The sequences are useful for the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease associated with the NOVX protein, or for diagnosing and treating
 CC disorders associated with the NOVX protein, such as cancer, myelogenous
 CC leukemia, congenital neonatal autoimmune thrombocytopaenia,
 CC immunological disorders, allergy and infection, asthma, lung diseases,
 CC reproductive disorders, male and female reproductive diseases,
 CC haemangioma, deafness, liver cirrhosis, hepatitis C, gastric disorders,
 CC diabetic retinopathy, psoriasis, multiple sclerosis, atherosclerosis,
 CC hypertension, stroke and heart failure. NOV10a represents a new member of
 CC the chemokine receptor family and the gene is located on chromosome 1.

XX

SQ Sequence 1119 BP; 258 A; 353 C; 220 G; 288 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,526-187 Length: 1119
 Score: 1967.00 Matches: 372
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-689-832-20 (1-372) x ADI79322 (1-1119)

QY 1 MetGluHisThrHisAlaHisLeuAlaAlaAenSerSerLeuSerTyrTyrSerProGly 20
 Db |||||
 QY 1 ATGGAGCACACGACGACCCCACTCGACGCCAACAGCTCGTCTTGTGGTGGTCCCGGC 60
 Db |||||
 QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
 Db |||||
 QY 61 TCGGCTCGGCTTGGGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
 Db |||||
 QY 41 LeuProAlaAenIleLeuThrValIleIleLeuSerGlnLeuValAlaAargGlnLys 60
 Db |||||
 QY 121 TTACCAGCAATAATCTTGACAGTGATCACTCTCCAGCTGGTGGCAAGACAGAGAG 180
 Db |||||
 QY 61 SerSerTyrAenTyrLeuLeuAlaAlaAlaAspIleLeuValLeuPhePheIle 80
 Db |||||
 QY 181 TCCTCTACAACTATCTTGGCACTCGTCTGCGACATCTTGGTCTCTTTTCATA 240
 Db |||||
 QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAenMetGlnMetProGlnValPro 100
 Db |||||
 QY 241 GTGTTTGGGACTTCTCTGTTGAAGATTTCATCTTGAACATGCAGATGCCTCAGGTCCC 300
 Db |||||
 QY 101 AspyIleIleGluValLeuGluPheSerSerIleHisThrSerIleThrIleThrVal 120
 Db |||||
 QY 301 GACAAGATCATAGAGTCTGGAATTCATCCATCCACCTCCATATGATGATTACTGTA 360
 Db |||||
 QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
 Db |||||
 QY 361 CGGTAAACCATTCACAGGTATATCGTCTGCGACCCCGCTCAAGTACCACACGGTCTCA 420
 Db |||||
 QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
 Db |||||
 QY 421 TACCCAGCCCGCACCCGAAAGTCAATTGTAAGTGTTTACATCACCTGCTGCTGACCCAGC 480
 Db |||||
 QY 161 IleProTyrTyrTyrTyrProAsnIleThrPheGluAspTyrIleSerThrSerValHis 180
 Db |||||
 QY 481 ATCCCTTATTACTGGTGGCCCAACATCTGGAGCTGAAGACTACATCAGCACCTCTGTGCAT 540
 Db |||||
 QY 181 HisValLeuIleTyrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
 Db |||||
 QY 541 CAGGTCTCTCATCTGGATCCACTGCTTACCGCTTACCTGGTGGTGGTGGTGGTGGTGG 600
 Db |||||
 QY 201 IleLeuAenSerIleIleValTyrLysLeuArgLysSerAsnAspPheArgLeuArgGly 220
 Db |||||
 QY 601 ATCTTGAACCTCAATCATTTGTGTACAAAGCTCAGGAGGAAGACAAATTTTCGTCTCG 660
 Db |||||
 QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
 Db |||||
 QY 661 TACTCCAGGGGAAGACACCGCCCATCTTGTTCACCATTTACCTCCATCTTTGCCACATT 720
 Db |||||
 QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyValAlaProIleGlnAsnArg 260
 Db |||||
 QY 721 TGGGCCCCCGCATCATCATGATCTTTTACCACTCTATGGGGCCCGCCATCCAGAACCGC 780
 Db |||||
 QY 261 TrpLeuValHisIleMetSerAspIleAlaAenMetLeuAlaLeuLeuAenThrAlaIle 280
 Db |||||
 QY 781 TGGCTGGTACACATCATCTCCGACATTCGCCAACATGCTAGGCCCTTCTGAAACACAGCCATC 840
 Db |||||
 QY 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
 Db |||||
 QY 841 AACTTCTTCTCTACTGCTTTCATGCAAGGGGTTCCGACCATGGAGCCCGCCAGCTC 900
 Db |||||
 QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
 Db |||||

Db 901 AAGCTTTCTCAAGTCCAGAACCACTGTACAGTTCTACACCAATCATAACTTTTCC 960
Qy 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 961 ATAACAAGTAGCCCTGGATCTCGCCGGCAAACTCACACTGCATCAAGATGCTGGGTAC 1020
Qy 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerSerTyrGln 360
Db 1021 CAGTATGACAAAAATGGAACACCTATAAAAGTCGTAATGACAGCAAAAGCTCTACCAG 1080
Qy 361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
Db 1081 TTGAGATGCCATTGGAGCTTGTGTGTCATCATCTG 1116

RESULT 4

ADO56001

ID ADO56001 standard; cDNA; 1119 BP.

XX

AC ADO56001;

XX

DT 15-JUL-2004 (first entry)

XX

DE DNA encoding human NOV10.

XX

KW human; gene; ss; cancer; obesity; diabetic nephropathy;

KW acute pancreatitis; stroke; multiple sclerosis.

XX

OS Homo sapiens.

XX

US2004058862-A1.

XX

PD 25-MAR-2004.

XX

PF 18-SEP-2002; 2002US-00246583.

XX

PR 18-SEP-2002; 2002US-00246583.

XX

PA (MAJU/) MAJUMDER K.

XX

PI Majumder K;

XX

DR WPI; 2004-268835/25.

XX

P-PSDB; ADO56002.

XX

Novel NOVX polypeptides, useful for treating cancer, obesity, diabetic

nephropathy, acute pancreatitis, strokes and multiple sclerosis.

XX

PS Claim 9; Page 26-27; 87pp; English.

XX

The invention relates to novel isolated NOVX nucleic acids and encoded polypeptides. The nucleic acids, polypeptides and antibodies raised against the polypeptides are useful for preventing or treating diseases associated with aberrant NOVX expression or activity e.g., cancer, CC obesity, diabetic nephropathy, acute pancreatitis, stroke, multiple sclerosis. The present sequence represents a NOVX nucleic acid of the CC invention.

XX

SQ Sequence 1119 BP; 258 A; 353 C; 220 G; 288 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,52e-187	Length:	1119
Percent:	1967.00	Matches:	372
Score:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-689-832-20 (1-372) x ADO56001 (1-1119)

Qy 1 MetGluHisThrHisAlaHisLeuAlaAlaAsnSerSerLeuSerTrpTrpSerProGly 20
Db 1 ATGGAGCAGCAGCCACCTCGCAGCCAAACAGCTCGCTGTCTTGGTGGTCCCCCGGC 60

RESULT 5

Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 61 TCGGCTCGCGCTGGGTTTCGTGCCGCGGTCTACTACAGCCTCTTGTGTGCTCGGT 120
Qy 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaArgArgGlnLys 60
Db 121 TTACCAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAGAGACAGAAG 180
Qy 61 SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
Db 181 TCCTCTTACACTATCTCTTGGCACTCGCTGCTGCCGACATCTTGGTCTCTTTTCATA 240
Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 241 GTGTTTGTGGACTTCTCTTGGAAAGATTTTCATCTTGAACATGACAGTGGCTCAGGTC 300
Qy 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
Db 301 GACAAGATCATAGAAGTGTGGAAATCTCATCATCCACCTCCATATGGATTACTGTA 360
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db 361 CCGTTAAACCATTTGACAGGTATATCGCTGCTGCCACCGCTCAAGTACCACAGGCTCA 420
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 421 TACCCAGCCCGCACCGGAAAGTCATTGTAAGTGTTTTACATCACCTGCTTCTCTGACG 480
Qy 161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
Db 481 ATCCCCCTATTACTGGTGGGCCCAACATCTGAGCTGGAAGACTACATCAGCACTCTGTGCAT 540
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 541 CAGCTCTCATCTGGATCCACTGCTTACCGTCTACTGCTGGTGGCTGCTCCATCTTCTTC 600
Qy 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
Db 601 ATCTTGAACATCAATCATTTGTGTACAAGCTCAGAGGAGAGAGCAATTTTCTGCTCCG 660
Qy 221 TyrSerThrGlyThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 661 TACTCCAGGGGAGAACACCCGCCATCTTGTTCACCATTTACCTTCCATCTTTGCACTT 720
Qy 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyValProIleGlnAsnArg 260
Db 721 TGGGCCCCCGCATCATCATGATTTCTTTACCACTCTATGSGGGGCGCATCCAGAACCG 780
Qy 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 781 TGGCTGGTACACATCATGTCCGACATTTGCCAATGCTAGCCCTTCTGAACACAGGCATC 840
Qy 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 841 AACTTCTTCTCTACTGCTTCATCAGCAAGCGGTTCCGCCACCATGGCAGCCGCGCTC 900
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 901 AAGGCTTCTTCAAGTGGCCAGAGCAACCTGTACAGTTCTACACCAATCATAACTTTTC 960
Qy 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 961 ATAACAAGTAGCCCTCGGATCTCGCCGGCAAACTCACACTGCATCAAGATGCTGGTGTAC 1020
Qy 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerSerTyrGln 360
Db 1021 CAGTATGACAAAAATGGAACACCTATAAAAGTCGTAATGACAGCAAAAGCTCTACCAG 1080
Qy 361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
Db 1081 TTGAGATGCCATTGGAGCTTGTGTGTCATCATCTG 1116

AAD29672
 ID AAD29672 standard; cDNA; 1130 BP.
 XX
 AC AAD29672;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human G-protein coupled receptor (GCRC-6) cDNA.
 XX
 KW Human; G-protein coupled receptor; GCRC-6; cell proliferative disorder;
 KW neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;
 KW metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;
 KW Pick's disease; Huntington's disease; Parkinson's disease; hypertension;
 KW atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytotoxic;
 KW osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening;
 KW transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant;
 KW neurotropic; neuroprotective; cardiant; immunosuppressive; anorectic;
 KW viricide; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 12..1130
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 FT sig_peptide 12..152
 FT /*tag= b
 FT mat_peptide 153..1127
 FT /*tag= c
 FT /product= "Human mature GCRC-6"
 FT
 XX WO200210387-A2.
 XX
 XX 07-FEB-2002.
 PD
 XX
 XX 25-JUL-2001; 2001WO-US023433.
 XX
 XX 27-JUL-2000; 2000US-0221478P.
 XX 03-AUG-2000; 2000US-0223268P.
 XX 21-AUG-2000; 2000US-0227054P.
 XX 08-SEP-2000; 2000US-0231121P.
 XX 13-SEP-2000; 2000US-0232243P.
 XX 15-SEP-2000; 2000US-0232691P.
 XX 22-SEP-2000; 2000US-0235146P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
 PI Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Wallia NK, Hafalia AJA;
 PI Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Gaul RC;
 PI Warren BA, Lee EA, Ding L;
 XX
 XX WPI; 2002-188744/24.
 DR P-PSDB; AAE18645.
 XX
 XX New human G-protein coupled receptor polypeptide for diagnosis,
 PT prevention and treatment of cell proliferative, neurological,
 PT cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
 PT disorders.
 XX
 XX Claim 5; Page 141; 150pp; English.
 PS
 XX The invention relates to novel human G-protein coupled receptors (GCRC)
 CC and their encoding polynucleotides. GCRC is useful as an immunogen for
 CC preparing monoclonal and polyclonal antibodies. GCRC is useful for
 CC diagnosing, treating and preventing a cell proliferative disorder (e.g.,
 CC hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy,
 CC Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's
 CC disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension,
 CC myocardial infarction), gastrointestinal disorder (e.g., gastritis,
 CC cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g.,
 CC acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma,

CC rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity,
 CC osteoporosis), and viral infections. GCRC is useful in a number of drug
 CC screening techniques, and to analyse the proteome of a tissue or cell
 CC type. GCRC is useful for creating knockin humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene
 CC therapy, to generate a transcript image of a tissue or cell type, for
 CC detecting differences in the chromosomal location due to translocation,
 CC inversion, etc., among normal, carrier or affected individuals, and as
 CC hybridization probes for mapping naturally occurring genomic sequences.
 CC GCRC is useful in Southern or northern analysis, dot blot or other
 CC membrane-based technologies, in PCR technologies, in dipstick, pin,
 CC multi-format enzyme linked immunosorbant (ELISA)-like assays, and in
 CC microarrays utilising fluids or tissues from patients to detect altered
 CC GCRC expression. The present sequence is human GCRC-6 cDNA
 XX
 SQ Sequence 1130 BP; 258 A; 357 C; 226 G; 289 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,55e-187 Length: 1130
 Score: 1967.00 Matches: 372
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
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 QY 1 MetGluHisThrHisAlaHisLeuAlaAlaHisSerSerLeuSerThrTrpSerProGly 20
 DB 12 ATGGAGCACACGACGCGCCACCTCGCAGCCACACGCTCGCTGCTTGGTGGTCCCGGC 71
 QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuCysLeuGly 40
 DB 72 TCGGCTCGCGCTGGGGTTTGGTGGTCTACTACAGCCTCTTCTGTGCTCGGT 131
 QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaArgGlnLys 60
 DB 132 TTACAGCAATATCTTGACAGTGNATCTCTCCAGCTGGTGGCAGAGACAGAG 191
 QY 61 SerSerTyrAsnTyrLeuLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
 DB 192 TCCTCCTACAACTATCTCTGGCACTCGCTGCGCACATCTTGGTCTCTTTTCATA 251
 QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
 DB 252 GTGTTTGGACTTCTCTTGGAGATTTCATCTTGAACATGCGAGATGCTCAGGTCC 311
 QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleThrIleThrVal 120
 DB 312 GACAGATCATAGAGTCTGGATTTCTATCCATCCACACTCCATATGGATTACTGTA 371
 QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
 DB 372 CCGTTAACCAATTGACAGGTATATCGCTGTCGCCACCGCTCAAGTACACACGCTCTCA 431
 QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
 DB 432 TACCAGCCCGACCCGGAAAGTCAATTGTAAGTGTTCATACACCTGCTTCTGACACG 491
 QY 161 IleProTyrTyrTrpProAsnIleThrThrGluAspTyrIleSerThrSerValHis 180
 DB 492 ATCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGACCTCTGTGGAT 551
 QY 181 HisValLeuIleThrPheHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
 DB 552 CACGCTCTCATCGATCCACTGCTTACCGTCTACCTGGTGGTGGTGGTGGTGGTGGT 611
 QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220
 DB 612 ATCTTGAACCTCAATCTGTGTAGAGCTCAGGAGGAGAGCAATTTTCGTCTCGGTGGC 671
 QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240


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Db 1467 TACCACGCCGCCACCGGAAAGTCATTGTAAAGTGTTTACATCAGCTGCTTCCTGCACGCG 1526
Qy 161 IleProTyrTyrTrpTrpProAnniIleTrpThrGluaspTyrIleSerThrSerValHis 180
Db 1527 ATCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 1586
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 1587 CAGTCTCATCTGGATCCATCTGCTTCCACCGTCTACTGGTGGCCCTGCTCCATCTTCTTC 1646
Qy 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220
Db 1647 ATCTGAACCAATCATTTGTGTACAAGCTCAGGAGGAAGCAATTTTGTCTCCGTGGC 1706
Qy 221 TyrSerThrGlyLysThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 1707 TACTCCACGGGGAGACCAACCGCATCTTGTTCACCATTTACCTCCATCTTTGCGACACTT 1766
Qy 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
Db 1767 TGGGCCCCCGCATCATCATGATCTTTTACCACCTCTATGGGGCGCCCATCCAGAACC 1826
Qy 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 1827 TGGCTGGTACACATCATGTCGACATTTGCCAATGCTAGCCCTTCTGAACACAGCCATC 1886
Qy 281 AspPheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 1887 AACTCTTCTCTACTGCTTTCATCAGCAAGCGGTTCGCACCATGCGCAGCGCCGCTC 1946
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 1947 AAGCTTTCTTCAAGTGGCCAGAGCAACCTGTGAAGTTCTACACCAATCATACTTTTC 2006
Qy 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 2007 ATAACAAGTAGCCCTGGATCTCGCCGGCAAACTCACACTGCATCAAGATGCTGGTGATC 2066
Qy 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerSerTyrGln 360
Db 2067 CAGTATGACAAAATGGAAAACCTATAAAAAGTCGTAAATGACAGCAAAAGCTCTTACCAG 2126
Qy 361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
Db 2127 TTTGAAGATGCCATTGGAGCTTGTGTCACTCACTCTG 2162
```

RESULT 7

ACF05276
ID ACF05276 standard; cDNA; 1110 BP.

XX ACF05276;

XX 06-NOV-2003 (first entry)

XX Human G-protein coupled receptor HGRPMY34 variant cDNA.

XX HGRPMY34; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;
XX human; neuroprotective; nootropic; tranquilizer; antimigraine;
XX neuroleptic; antianemic; antidepressant; anticonvulsant; antiparkinsonian;
XX cytotatic; cardiac; hypotensive; antianginal; analgesic; anorectic;
XX anti-HIV; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic;
XX gene therapy; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX 1. .1110

XX CDS /tag= a
XX /product= "HGRPMY34 variant"

XX WO2003050256-A2.

XX 19-JUN-2003.

PD

XX

PF 06-DEC-2002; 2002WO-US039290.

XX 06-DEC-2001; 2001US-0338371P.

PR (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Feder JN, Gopal S, Mintier GA, Ramanathan CS;

PI WPI; 2003-577295/54.

XX P-PSDB; ABR62522.

DR New nucleic acid molecule encoding a human G-protein coupled receptor,

XX HGRPMY34, useful for diagnosing, preventing or treating diseases

PT involving the receptor, for example Parkinson's disease, dementia,

PT asthma, hypertension or cancer.

PT Claim 1; Fig 2A-B; 112pp; English.

XX The present sequence is that of cDNA encoding a variant of human

CC HGRPMY34 containing a deletion of 3 amino acids of the protein sequence

CC but expected to share at least some of the expression patterns and

CC function of HGRPMY34. This is a newly identified G-protein coupled

CC receptor (GPCR) belonging to the group of 'Class A' GPCRs and showing

CC homology to the Pfam model 7 transmembrane receptor, rhodopsin family.

CC HGRPMY34 (or GPCR-P14, GPCR-145) is highly expressed in brain (amygdala,

CC caudate nucleus, corpus callosum, hippocampus, thalamus, substantia

CC nigra), spinal cord and pituitary, indicating an association in

CC neurological systems and conditions. It is also expressed in the bone

CC marrow and testis. The invention provides HGRPMY34 polynucleotides,

CC polypeptides and antibodies, expression vectors, host cells and antisense

CC molecules, methods for screening for modulators of HGRPMY34 activity

CC and/or function, and methods for diagnosing, treating, preventing and

CC screening for disorders and diseases associated with abnormal HGRPMY34

CC activity, including: a disorder related to aberrant G-protein coupled

CC signalling; a disorder related to aberrant cell cycle regulation;

CC neurological disorders; anxiety; headache; migraine; schizophrenia; manic

CC depression; delirium; dementia; severe mental retardation and

CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's

CC syndrome; Parkinson's disease; brain disorders; spinal cord disorders;

CC affective disorders; neoplastic disorders; cardiovascular disorders;

CC acute heart failure; hypotension; hypertension; angina pectoris;

CC myocardial infarction; an immunological disorder; immune-related

CC disorders; endocrinal diseases; growth disorders; neuropathic pain;

CC obesity; anorexia; HIV infections; cancers; bulimia; asthma; osteoporosis

CC ; psychosis; metabolic disorders; pituitary disorders; urinary retention;

CC ulcers; allergies; or benign prostatic hypertrophy (all claimed)

XX SQ Sequence 1110 BP; 253 A; 351 C; 220 G; 286 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.43e-184 Length: 1110
Score: 1939.50 Matches: 369
Percent Similarity: 99.19% Conservative: 0
Best Local Similarity: 99.19% Mismatches: 0
Query Match: 98.60% Indels: 3
DB: Gaps: 1

US-10-689-832-20 (1-372) x ACF05276 (1-1110)

Qy 1 MetGluHisThrHisAlaHisLeuAlaAAsnSerSerLeuSerTrpTrpSerProGly 20
Db 1 ATGGAGCACACGACGCCACCTCGCAGCAACAGCTCGCTGTGTGGTGGTCCCCCGGC 60
Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 61 TCGGCTCGGGCTTGGGTTTCGGTTCGGCCGGTGTACTACAGCTCTTGTGTGCTCGGT 120
Qy 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaArgGlnLys 60
Db 121 TTACCAGCAAAATATCTTGACAGTATCATCTCTCCAGCTGTGTGGCAGAGACAGAAAG 180
Qy 61 SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80

Db 181 TCCTCTTACAACTATCTCTTGCCACTCGCTGCTGCCGACATCTTGCTCTCTTTTCATA 240
Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 241 GTGTTTGTCGACTCTCTGTTGGAGATTTCATCTTGAAATGATGATGCTCAGGTCC 300
Qy 101 AspLysIleLeuGluValLeuGluPheSerSerIleHisThrSerIleThrVal 120
Db 301 GACAAATCATAGAGTGTGGATTCTCATCATCCACACCTCCATATGATTACTGTA 360
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db 361 CCGTTAACCAATTGACAGGTATATCGCTGTCTGCCACCCGCTCAAGTACCACACGGTCTCA 420
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 421 TACCCAGCCCGACCCGGAAGTCAATGTGAAGTGTATACATCACTGCTTCTTGACACG 480
Qy 161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
Db 481 ATCCCTATTACTGTTGGCCCAACATCTGCACTGAAGACTTACATCAGCACCTCTGTGCAT 540
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 541 CAGCTCTCATCTGGATCCACTGCTTACCGTCTACCTGGTGCCTGCTCCATCTTCTTTC 600
Qy 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220
Db 601 ATCTTGAACTCAATCATGTGTGAACAGCTCAGGAGGAAGCAATTTGCTCTCCGTGGC 660
Qy 221 TyrSerThrGlyLysThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 661 TACTCCAGCGGGAAGACACCGCACTTGTTCACCATTTACCTCCATCTTGGCACACTT 720
Qy 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
Db 721 TGGGCCCCCGCATCATCATGATTTTACCACCTCTATGGGCGGCCCATCCAGAACCGC 780
Qy 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 781 TGCTGTGACATCATCATGATCCGACATTCGCACATGCTAGCCCTCTTGAAACAGCGCATC 840
Qy 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 841 AACTCTTCTCTACTGCTTCATCAGCAAGCGGTTCCGACCATGCGACGCGCCACGCTC 900
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 901 AAGGCTTTCTCAAGTGCAGAGCAACCTGTACAGTTCTTACACCAATCATTAACCTTTTC 960
Qy 321 IleThrSerSerProTyrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 961 ATAAAGTAGTCCCTGATCTCGCGCAAACTCACATGCAATCAAGATGCTGGGTAC 1020
Qy 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerTyrGln 360
Db 1021 CAGTATGACAAAATGGA-----AAAGTGTGTAATGACAGCAAAAGCTCTTACCAG 1071
Qy 361 PheGluAspAlaIleGlyAlaCysValIleLeu 372
Db 1072 TTGGAAGATGCCATTGGAGCTTGTGTCATCATCTCTG 1107

RESULT 8

ADD18120

ID ADD18120 standard; DNA; 2189 BP.

XX

AC ADD18120;

XX 15-JAN-2004 (first entry)

DT Human G-protein coupled receptor (GPCR) DNA sequence Seq ID6.

XX

KW G protein coupled receptor; GPCR; signal transduction pathway; G protein;
KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
KW colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
KW sleeplessness; hypertension; anxiety; stress; renal failure;
KW cardiovascular disorder; neural disorder; oncology disorder;
KW immune disorder; neuroprotective; gene therapy; gene; ds.
XX Homo sapiens.
XX OS
XX PH
XX FT
FT CDS
FT 1047..2157
FT /*tag= a
FT /product= "Human G-protein coupled receptor"
FT /transl_except= (2085..2091, aa:KPIKS)
XX
PN WO2003016478-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 15-AUG-2002; 2002WO-US026017.
XX
XX PR 20-AUG-2001; 2001US-0313658P.
XX PR 12-SEP-2001; 2001US-0318675P.
XX PR 30-OCT-2001; 2001US-0340703P.
XX PR 26-NOV-2001; 2001US-0333417P.
XX PR 06-DEC-2001; 2001US-0338367P.
XX PR 06-FEB-2002; 2002US-0355596P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX PI Feder JN, Ramanathan CS, Gopal S, Mintier GA;
XX WPI: 2003-278558/27.
XX P-PSDB; ADD18023.
XX
XX PT New nucleic acid, useful for manufacturing a medicament for preventing,
XX treating or ameliorating a medical condition e.g., neural disorder.
XX
XX PS Example 2; SEQ ID NO 6; 251pp; English.
XX
XX CC This invention relates to novel G protein coupled receptors (GPCRs) and
XX their encoding nucleotide sequences. Many medically significant
XX biological processes are mediated by proteins participating in signal
XX transduction pathways involving G proteins. GPCRs are one of the largest
XX receptor superfamilies known. These receptors are biologically important
XX and malfunction of these receptors results in diseases such as
XX Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal
XX pigmentosa and asthma. They are also involved in depression,
XX schizophrenia, sleeplessness, hypertension, anxiety, stress, renal
XX failure and other cardiovascular, neural, oncology and immune disorders.
XX A modulator of the GPCRs of the invention may have neuroprotective
XX activity whilst the sequences of the invention may be useful for gene
XX therapy. The invention may also be useful for manufacturing a medicament
XX for preventing, treating or ameliorating a medical condition. The present
XX sequence is the DNA sequence encoding a human GPCR of the invention.
XX
SQ Sequence 2189 BP; 451 A; 691 C; 581 G; 466 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.64e-184 Length: 2189
Score: 1939.50 Matches: 369
Percent Similarity: 99.19% Conservatives: 0
Best Local Similarity: 99.19% Mismatches: 0
Query Match: 98.60% Indels: 3
DB: 10 Gaps: 1

US-10-689-832-20 (1-372) x ADD18120 (1-2189)

Qy 1 MetGluHisThrHisAlaHisLeuAlaAsnSerSerLeuSerTrpTrpSerProGly 20

Db 1047 ATGGAGCACACACACGACCCACCTCGACGCAACAGCTCGTGTGTGGTGGTCCCGGC 1106

Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40

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Db      1107 TCGGCTGGGCTTGGGTTCTGCGCGTGGTCTACTACAGCCTCTTGTGTGCTCGGT 1166
QY      41  LeuProAlaAsnIleuThrValIleleLeuSerGlnLeuValAlaAargGlnIys 60
Db      1167 TTACGAGCAAAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGAAGACAGAAG 1226
QY      61  SerSerTyrAsnTyrLeuLeuAlaAlaAspIleLeuValIleuPhePheIle 80
Db      1227 TCTCTCTCAACATATCTCTTGGCATCGCTGCTGCCGACATCTTGGTCTCTTTTCATA 1286
QY      81  ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db      1287 GGTGTTGTGGACTTCTCTGTGGAGATTTCATCTTGAACATGCAGATGCCTCAGTCCCC 1346
QY      101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTyrIleThrVal 120
Db      1347 GACAAAGATCATAGAAGTGTGGAATTCATCATCCATCCACACCTCCATATGGATTACTGTA 1406
QY      121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db      1407 CGGTTAACCAATTGACAGGTATATCGTGTGCCACCGCGTCAAGTACCAACAGGTCTCA 1466
QY      141  TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db      1467 TACCAGCCGCGACCCGGNAAGTCATTGTAGTGTTTACATCACCTGTTCTGTGACGAGC 1526
QY      161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
Db      1527 ATCCCTATTACTGTGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 1586
QY      181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db      1587 CAGTCTCATCTGATCAGTCCATCCCTGTCACCGTCTACCTGGTGGCCCTGTCTCCATCTTTC 1646
QY      201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
Db      1647 ATCTTGACTCAATCATTTGTGTACAGCTCAGAGAGAGAGCANTTTTGTCTCGCTGGC 1706
QY      221 TyrSerThrGlyLeuThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db      1707 TACTCCAGGGGAGACACCGCCATCTTGTTCACCATTTACCTCTTTGCCACACTT 1766
QY      241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
Db      1767 TGGGCCCCCGCATCATCATGATTCTTTACCACTCTATGGGGCCGCCATCCAGAACCGC 1826
QY      261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db      1827 TGGCTGGTACACATCATGTCCGACATTTGCCAATGCTTAGCCCTTCTGACACAGCCATC 1886
QY      281 AsnPheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaAlaThrLeu 300
Db      1887 AACTTCTTCTCTACTGCTTTCATCAGCAAGCGGTTCCGACCATGGCAGCGCCACGCTC 1946
QY      301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db      1947 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGATTCTACCAACATCATAACTTTTCC 2006
QY      321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db      2007 ATAAACAGTAGCCCTTGGATCTCGCGCGCAAACTCACACTGCATCAAGATGCTGTGTAC 2066
QY      341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerSerTyrGln 360
Db      2067 CAGTATGACAAAATGGA-----AAAAGTCGTAATGACAGCAAAAGCTCTTACCAG 2117
QY      361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
Db      2118 TTGAAGATGCCATTGGAGCTGTGTGCATCATCTG 2153
```

RESULT 9
ADRI6433

```
ID      ADRI6433 standard; cDNA; 2117 BP.
XX
AC      ADRI6433;
XX
DT      04-NOV-2004 (first entry)
XX
DE      Human KOR3-like (KOR3L) cDNA.
XX
KW      Human; KOR3-like; KOR3L; gene; ss; G-protein coupled receptor; GPCR;
KW      loss of balance; sensorimotor integration; obesity; anorectic.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      CDS 280..1341
FT      /*tag= a
FT      /product= "Human KOR3L protein"
XX
PN      US2004161799-A1.
XX
PD      19-AUG-2004.
XX
PF      13-FEB-2004; 2004US-00779104.
XX
PR      14-FEB-2003; 2003US-0447447P.
PR      14-AUG-2003; 2003US-0495577P.
XX
XX      (MURP/) MURPHY A J.
XX      (CROLL/) CROLL-KALISH S.
XX
PI      Murphy AJ, Croll-Kalish S;
XX
DR      WPI; 2004-593074/57.
DR      P-PSDB; ADRI6434.
XX
XX      Identifying an agent capable of modulating a KOR3-like protein (a class
XX      of G-protein coupled receptor protein), useful for treating
XX      obesity, comprises contacting agent with KOR3like protein and detecting
XX      binding.
XX
XX      Disclosure; SEQ ID NO 1; 16pp; English.
XX
XX      The invention relates to a method for identifying an agent capable of
XX      modulating activity of a KOR3-like (KOR3L) protein (a class of G-protein
XX      coupled receptor protein (GPCR)) or protein fragment, involving
XX      contacting a test agent with a KOR3L protein or protein fragment and
XX      determining the ability of the test agent to bind the KOR3L protein or
XX      protein fragment. The invention also relates to a method of treating
XX      KOR3L-mediated loss of balance or sensorimotor integration by
XX      administering an agent capable of activating KOR3L, a method of treating
XX      obesity involving administering an agent capable of inhibiting KOR3L, a
XX      pharmaceutical composition comprising an agent identified by a method of
XX      the invention and a carrier, and a transgenic animal comprising a
XX      modification of an endogenous KOR3L gene. The methods of the invention
XX      are useful for identifying an agent capable of modulating a KOR3L
XX      protein. The agent is useful for treating KOR3L mediated loss of balance
XX      or sensorimotor integration, and for treating obesity. This sequence
XX      represents cDNA encoding the human KOR3L protein of the invention.
XX
SQ      Sequence 2117 BP; 490 A; 625 C; 497 G; 505 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,33e-181 Length: 2117
Score: 1907.00 Matches: 372
Percent Similarity: 83.22% Conservative: 0
Best Local Similarity: 83.22% Mismatches: 0
Query Match: 96.95% Indels: 75
DB: 13 Gaps: 1

US-10-689-832-20 (1-372) x ADRI6433 (1-2117)

QY      1 MetGluHisThrHisAlaHisLeuAlaAsnSerSerLeuSerTrpTrpSerProGly 20
|||||
```

280	ATGGAGCACACGACGCCACCTCGACGCCAACAGCTCGCTGTCTTGTGTGTGTCCTCCCGGC	339
21	SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly	40
340	TCGGCCTCGCGCTTGGGTTTCGTGCCGTGTCTACTACAGCCTCTTGTGTGCTCGT	399
41	LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAraGrgGlnLys	60
400	TTACCAGCAAAATATCTTGACAGTGATCATCTCTCCCAAGCTGGTGGCAAGAAGACAGAAG	459
61	SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAaspIleLeuValLeuPhePheIle	80
460	TCCTCTCAACAATACTCTTGCGACTCGCTGTCGCGACATCTTGGTCCTCTTTTTCATA	519
81	ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro	100
520	GTGTTTGTGGACTTCTCTGTGGAGATTTCATCTTGAACATGCAGATGCCTCAGTCCCC	579
101	AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrrIleThrVal	120
580	GACAAGATCATAGAAGTGTGGAAATTTCTCATCTCCATCCACACTCCATATGATTTACTGTA	639
121	ProLeuThrIleAspAraGlyIleAlaValCysHisProLeuLysTyrHisThrValSer	140
640	CCGTTAACCATTGACAGGTATTCGTGTCTGCCACCGCTCAAGTACACACCGGTCTCA	699
141	TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer	160
700	TACCCAGCCGACCCCGAAGTCATTGTAAGTGTTTACATCATCTGCTTCTGCACGAC	759
161	IleProTyrTyrTrrPrrProAsnIleTrrPrrGluAspTyrIleSerThrSerValHis	180
760	ATCCCTCATTAATCTGGTGCCCAACATCTGGAGTCAAGACTACATCAGCACCTCTGTGCAT	819
181	HisValLeuIleTrrIleHisCysPheThrValTyrIleuValProCysSerIlePhePhe	200
820	CACGTCTCATCTGGATCCACTGTTTACCGTCTACCTGGTGCCCTGCTCCATCTTCTTC	879
201	IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly	220
880	ATCTTGAATCAATCATTTGTGTACAAGCTCAGGAGGAAGACATTTTGGTCTCCGTGGC	939
221	TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu	240
940	TACTCCACGGGGAAGACACCGCCATCTTGTGTTCACCATTACTCCATCTTGTCCACACTT	999
241	TrrAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg	260
1000	TGGGCCCCCGCATCATCATGATTTCTTACCACTCTATGGGGCGCCATCCAGAACCGC	1059
261	TrrLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle	280
1060	TGGCTGTGTGCACATCATGTCCGACATTTGCCAACATGTAGCCCTTCTGAAACAGACCATC	1119
281	AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu	300
1120	AACTTCTTCTCTACTGCTTCATCAGCAAGCGGTTCGGCACCATGGCGAGCGCCACGCTC	1179
301	LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer	320
1180	AAGCTTCTTCAAGTGCAGAACACCTGTGACAGTCTATACCAATCATAACTTTTTC	1239
321	IleThrSerSerProTrrPrrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr	340
1240	ATAACAAGTAGCCCTGGATCTCGCCGGCAAACTCACACTGCATCAGATGCTGGTGTAC	1299
341	GlnTyrAspLysAsnGlyLysProIle-Lys-	350
1300	CAGTATGACAAAAATGGAACACCTATAAAGATATCCCGTGATTCATAGGTGTGGCAAC	1359
350	-----	350
1360	TACTGCCTCTGTCTAAATCCATTTCCAGATGGGAAGGTGTCCATCTTATGGCTGAGCAGC	1419

PI Vernet CAM;
 XX WPI; 2001-639127/73.
 DR P-PSDB; AAU10068.
 XX
 PT Polypeptides and nucleic acids related to chloride channel, insulin-like
 PT growth factor family of proteins, useful for diagnosing and treating
 PT cancer, cystic fibrosis, acute pancreatitis and Alzheimer's disease.
 XX
 XX Claim 9; Page 44; 15ipp; English.
 PS
 SS The invention describes isolated NOVX (NOVX1-11) polypeptides. NOVX
 CC polypeptides are useful for treating pathology associated with NOVX
 CC polypeptides, determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX, identifying agents binding to
 CC NOVX and treatment of disorders associated with altered expression of
 CC members of chloride channel-associated proteins e.g. cystic fibrosis and
 CC congenital myotonia. NOVX proteins are useful in treatment of disorders
 CC including psoriasis, cancer, diabetes, metabolic disorders of pancreas,
 CC e.g. acute pancreatitis, abnormal growth and accumulation of mast cells
 CC in one or more organs (e.g. haemophilia, anaemia), Fendred syndrome,
 CC skeletal dysplasias, disorders characterised by altered cell shape,
 CC motility, and apoptosis, ischaemic injury, hepatitis, neuroepithelial
 CC disorders, hepatic disorders (e.g. cryptogenic cirrhosis) and in the
 CC treatment of disorders of vascular smooth muscle cell differentiation,
 CC (e.g. heart failure, stroke). NOVX nucleic acids and polypeptides are
 CC useful to screen for molecules which inhibit or enhance NOVX activity or
 CC function and are useful as targets for the identifying small molecules,
 CC that modulate or inhibit e.g. neurogenesis, proliferation, motility, cell
 CC differentiation, haematopoiesis, wound healing and angiogenesis. NOV
 CC sequences are also useful for: identifying a cell or tissue type in a
 CC biological sample; amplifying DNA sequences from very small biological
 CC samples e.g. hair or skin or body fluids and as primers and probes to
 CC identify and/or clone NOVX homologues. NOVX proteins are useful
 CC immunogens to generate antibodies to monitor protein levels and modulate
 CC NOVX activity. Cells comprising the nucleic acids are useful for
 CC producing transgenic animals, for studying the function and/or activity
 CC of NOVX protein and identifying and/or evaluating modulators of NOVX
 CC protein activity. This sequence encodes NOVX1 (located on chromosome 1)
 CC related to the chemokine receptor family of proteins, one of 12 NOV
 CC polypeptides described in the method of the invention
 XX
 SQ Sequence 1343 BP; 315 A; 403 C; 273 G; 352 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.52e-181 Length: 1343
 Score: 1903.00 Matches: 371
 Percent Similarity: 83.00% Conservative: 0
 Best Local Similarity: 83.00% Mismatches: 1
 Query Match: 96.75% Indels: 75
 DB: 4 Gaps: 1
 US-10-689-832-20 (1-372) x AAS15731 (1-1343)
 QY 1 MetGluHisThrHisAlaHisLeuAlaAlaAanSerLeuSerTrpTrpSerProgly 20
 DB 2 ATGGAGACACGACGCCACCTCGACGACACAGCTCGCTGTTGGTGGTCCCCCGGC 61
 QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTrpSerLeuLeuLeuLeuGly 40
 DB 62 TCGGCTCGGGCTTGGTTCGTGGCGGTGCTACTACAGCCCTCTTGTGCTCGGT 121
 QY 41 LeuProAlaAanIleuThrValIleIleLeuSerGlnLeuValAlaAArgGlnLys 60
 DB 122 TTACAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAG 181
 QY 61 SerSerTrpAsnTyrLeuLeuAlaLeuAlaAlaAAspIleLeuValIlePhePheIle 80
 DB 182 TCCTCTAACAATATCTCTTGGCACTCGCTGCTGCCGACATCTTGGTCTCTTTTCATA 241
 QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAanMetGlnMetProGlnValPro 100
 DB 242 GTGTTGTGGACTTCTCTGTGGAGATTTTCATCTTGAACATGCAGATGCCTCAGGTCCC 301

QY 101 AsplysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
 DB 302 GACAAGATCATAGAAAGTCTGGAATTTCTCATCCATCCACACCTCATATGATGATCTGTA 361
 QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
 DB 362 CCGTTAACCATTTGACAGGTATATCATCTGTCTGCCACCGCTCAAGTACCAACACGGTCTCA 421
 QY 141 TyrProAlaAargThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
 DB 422 TACCAGCCGCGACCCGGAAGTCAATTGTAAGTGTTTACATCACCTGCTCTCTGACCAGC 481
 QY 161 IleProTyrTyrTrpTrpProAanIleTrpThruAspTyrIleSerThrSerValHis 180
 DB 482 ATCCCTCTATTACTGCTGGCGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGAT 541
 QY 181 HisValLeuIleTyrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
 DB 542 CACGCTCTCATCTGGATCCACTGCTTACCCTCTACTGCTGGCGCTGCTCATCTTCTTC 601
 QY 201 IleLeuAanSerIleIleValTyrLysLeuAargLysSerAanPheAArgLeuAArgGly 220
 DB 602 ATCTTGAACCTCAATCATTTGTGTACAGCTCAGGAGGAAGAGCAATTTTCTGCTCGTGGC 661
 QY 221 TyrSerThrGlyLysThrThrAlaIleuPheThrIleThrSerIlePheAlaThrIleu 240
 DB 662 TACTCCACGGGGAAGACACCGCCATCTTGTTCACCATTTACTCCATCTTTGGCACACTT 721
 QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAanArg 260
 DB 722 TGGGCCCCCGCATCATCATGATTTCTTACCACCTCTATGGGGCGCCCATCCAGAACGC 781
 QY 261 TrpLeuValHisIleMetSerAspIleAlaAanMetLeuAlaLeuLeuAanThrAlaIle 280
 DB 782 TGGCTGTGTACATCATGTTCGACATTTGCCAACATGCTAGCCCTCTTGAACACAGCCATC 841
 QY 281 AsnPhePheLeuTyrCysPheIleSerIysAargPheArgThrMetAlaAlaThrIleu 300
 DB 842 AACTTCTTCTCTACTGCTCTCATCAGCAAGCGGTTCGACACCATGCGGACGCCGCGCTC 901
 QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAanPheSer 320
 DB 902 AAGCTTTTCTTCAAGTGGCAGACACCTGTACAGTTCTACACCAATCATATCTTTTCC 961
 QY 321 IleThrSerSerProTrpIleSerProAlaAanSerHisCysIleLysMetLeuValTyr 340
 DB 962 ATAACAAGTAGCCCTGGATCTCGCGGCAAACTCACACTGCAATCAAGATGCTGGTGTAC 1021
 QY 341 GlnTyrAspLysAanGlyLysProIle-Lys----- 350
 DB 1022 CAGTATGACAAAAATGGAAAACTTATAAAGTATATCCCGGTGATTCATAGGTGGGCAAC 1081
 QY 350 ----- 350
 DB 1082 TACTGCCTCTGTCTAATCCATTTCCAGATGGGAAGGTGCCCATCTCTATGGCTGAGCAGC 1141
 QY 350 ----- 350
 DB 1142 TCTCCTTAAGAGTCTAATCCGATTTCTGCTCTCCCGCAGACTGGGCAATTTCTCAGACTG 1201
 QY 350 ----- 350
 DB 1202 GTAGATGAGAAGAGATGGAGAGAGAAAGAGAGCATGAAGCTGTTTGTATTATGCA 1261
 QY 351 -----SerArgAanAspSerLysSerSerTyrGlnPheGluAspAlaIle61 366
 DB 1262 TTTATTTCCACAGAGTGTATATGACAGCAAAAGCTCTACAGTTTGAAGATGCCATTGG 1321
 QY 366 YAlaCysValIleIleLeu 372
 DB 1322 AGCTTGTGTATCATCATCTG 1340

RESULT 11

ADJ87768

ID ADJ87768 standard; DNA; 1343 BP.

XX AC

ADJ87768;

XX DT

06-MAY-2004 (first entry)

XX DX

G-coupled protein receptor-related protein coding sequence #57.

XX DE

novel protein; G-coupled protein receptor-related protein; cardiomyopathy; atherosclerosis; cell signal processing-related disorder; metabolic pathway modulation-related disorder; diabetes; cancer; stroke; Huntington's disease; epilepsy; anxiety; pain; hypercholesterolemia; obesity; hypertension; Crohn's disease; systemic lupus erythematosus; viral infections; bacterial infection; parasitic infection; hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome; Alzheimer's disease; tuberculous sclerosis; hypercalcaemia; cerebral palsy; gene; ds.

XX OS

Unidentified.

XX SS

WO2002102321-A2.

XX PN

27-DEC-2002.

XX PD

18-JUN-2002; 2002WO-US019522.

XX PF

18-JUN-2001; 2001US-029899AP.

XX PR

18-JUN-2001; 2001US-0299134P.

XX PR

04-OCT-2001; 2001US-00972446.

XX PR

06-JUN-2002; 2002US-00299134.

XX PR

07-JUN-2002; 2002US-00298994.

XX PA

(CURA-) CURAGEN CORP.

XX PI

Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS;

XX PI

Pena CEA, Spaderna SK, Zhong M;

XX XX

WPI; 2003-167441/16.

XX DR

P-PSDB; ADJ87769.

XX DR

New MOLX polypeptides and polynucleotides, useful in gene therapy,

XX PT

particularly for treating or preventing e.g. cardiomyopathy,

XX PT

atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate

XX PT

cancer, stroke or pain.

XX PS

Claim 8; SEQ ID NO 203; 378pp; English.

XX CC

The invention comprises the amino acid and coding sequences of novel G-coupled protein receptor-related (MOL) proteins. The DNA and protein sequences of the invention are useful for treating or preventing a MOL-associated disorder, such as: cardiomyopathy, atherosclerosis, disorders associated with cell signal processing and metabolic pathway modulation, or diabetes. The DNA and protein sequences are also useful for the treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety, pain, hypercholesterolemia, obesity, hypertension, Crohn's disease, systemic lupus erythematosus, viral infections, bacterial infections, parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau syndrome, Alzheimer's disease, tuberculous sclerosis, hypercalcaemia, or cerebral palsy. The present DNA sequence encodes a MOL protein of the invention.

XX SQ

Sequence 1343 BP; 315 A; 403 C; 273 G; 352 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8,52e-181	Length:	1343
Score:	1903.00	Matches:	371
Percent Similarity:	83.00%	Conservative:	0
Best Local Similarity:	83.00%	Mismatches:	1
Query Match:	96.75%	Indels:	75
DB:	10	Gaps:	1

US-10-689-832-20 (1-372) x ADJ87768 (1-1343)

QY 1 MetGluHisThrHisAlaHisLeuAlaAlaHisSerSerLeuSerTrpTrpSerProGly 20

Db 2 ATGGAGCACACGACGCGCCACCTCGCAGCCACAGCTCGTGTCTTGGTGGTCCCGCGC 61

QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40

Db 62 TCGGCTCGCGCTTGGGTTTCTGTCGCCGTGTACTACTAGCCTTCTGTGSCCTCGGT 121

QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAargArgGlnLys 60

Db 122 TTACCGAAGAAATCTTTCAGAGTATCATCTCTCCAGCTGGTGGCAGAGACAGAG 181

QY 61 SerSerTyrAsnTyrLeuLeuAlaAlaAlaAspIleLeuValLeuPhePheIle 80

Db 182 TCCTCTCACTATCTCTTGGCACTGCTGCGCAGCATCTTGGTCTCTCTTTTCATA 241

QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100

Db 242 GTGTTTGTGGACTTCTCTTGAAGATTTCATCTTGAACATGCAGATGCCTCAGGTCCCC 301

QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120

Db 302 GACAGATCATAGAGTGTGGAATTCATCTCCATCCACCTCCATATGGATTACTGTA 361

QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140

Db 362 CGTTAACCATTTGACAGGTATATCATCTGTCTGCCACCGCTCAGTACCAACAGGTCTCA 421

QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160

Db 422 TACCAGCCGACCCCGGAAAGTCATTGTAAGTGTTTATACATCACCTGCTCTCTGACCAGC 481

QY 161 IleProTyrTyrTrpTrpProAsnIleThrGluAspTyrIleSerThrSerValHis 180

Db 482 ATCCCCATTATCTGTGTGGCCCAACATCTGGAGCTGAAGACTACATCAGCACCTCTGTGCAT 541

QY 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200

Db 542 CAGTCTCTCATCTGGATCCACTGTCTTACCGTCTACTTGGTGGCCCTGCTCCATCTCTTC 601

QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220

Db 602 ATCTTGAATCAATCATTTGTGTACAGCTCAGGAGGAAGAGCAATTTTTCGTCTCGTGGC 661

QY 221 TyrSerThrGlyLysThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240

Db 662 TACTCCAGGGGAAGACCCAGCCCATCTTGTTCACCATTTACTCTCCATCTTTGCCACACTT 721

QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260

Db 722 TGGGCCCCCGCATCATCATGATTTCTTACCACCTCTATGGGGCCGCCCATCCAGAACCGC 781

QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280

Db 782 TGGCTGGTACACATCATGTCTCCGACATTGCCAACATGCTAGCCCTTCTGAACACACCCATC 841

QY 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300

Db 842 AACTTCTTCTCTACTGTCTTCATCAGCAAGCGGTTCGCGCACCATGCGCAGCGCCAGCTC 901

QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320

Db 902 AAGGCTTTCTTCAAGTGCAGAGCACTGTACAGTTCTACACCAATCAATAACTTTTCC 961

QY 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340

Db 962 ATACAGTAGTACCCCTCGATCTCGCGGCAAACTCACACTGCATCAAGATGCTGTGTATC 1021

QY 341 GlnTyrAspLysAsnGlyLysProIle-Lys----- 350

Db 1022 CAGTATGACAAAAATGGAAAACTTATAAAGTATATCCCGGTGATCCATAGGTGTGGCAAC 1081

QY 350 ----- 350
 Db 1082 TACTGCTCTGTCTAATCCATTCCAGATGGAAGGTGCCATCCTATGCTGAGCAGC 1141
 QY 350 ----- 350
 Db 1142 TCTCCTTAAGAGTGCTAATCCGATTCTCTGCTCCCGCAGAGTGGCAATTCTCAGACTG 1201
 QY 350 ----- 350
 Db 1202 GTAGTAGAAGAGATGGAAGAGAAGAAAGAGAGCATGAAGCTTGTCTTACTTATGCA 1261
 QY 351 -----SerArgAsnAspSerLysSerSerTyrGlnPheGluAspAlaIleG1 366
 Db 1262 TTTATTTCCAGAGTCTGTATGACGCAAAAGCTCTACCAGTTTGAGATGCCAATGG 1321
 QY 366 yAlaCysValIleIleLeu 372
 Db 1322 AGCTTGTGTCATCATCCTG 1340
 RESULT 12
 ADI79324
 ID ADI79324 standard; DNA; 1343 BP.
 XX
 AC ADI79324;
 DT 22-APR-2004 (first entry)
 XX
 DE NOV11 coding sequence, SEQ ID 21.
 XX
 KW Cytostatic; Immunosuppressive; Antiallergic; Antimicrobial; Vasotropic;
 KW Respiratory; Hepatotropic; Virucide; Gastrointestinal; Antidiabetic;
 KW Ophthalmological; Antipsoriatic; Neuroprotective; Nootropic;
 KW Antiarteriosclerotic; Hypotensive; Cardiant; Cerebroprotective;
 KW Gene Therapy; NOVX; human; cancer; myelogenous leukaemia;
 KW congenital neonatal autoimmune thrombocytopaenia; immunological disorder;
 KW allergy; infection; asthma; lung disease; reproductive disorder;
 KW haemangioma; deafness; liver cirrhosis; hepatitis C; gastric disorder;
 KW diabetic retinopathy; psoriasis; multiple sclerosis; atherosclerosis;
 KW hypertension; stroke; heart failure; chromosome 1; NOV11;
 KW chemokine receptor; gene; ds.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH CDS
 FT 2..1063
 FT /*tag= a
 FT /product= "NOV11"
 XX
 FN WO2004009635-A2.
 XX
 PD 29-JAN-2004.
 XX
 PF 04-OCT-2001; 2001WO-US031292.
 XX
 PR 20-MAR-2001; 2001US-00813432.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;
 PI Vernet CAM;
 XX
 DR WPI; 2004-123380/12.
 DR P-PSDB; ADI79325.
 XX
 PS Claim 8; Page 43-44; 158pp; English.
 XX
 CC The present invention relates to novel NOVX proteins and their coding
 CC sequences (ADI79304-ADI79327). The sequences are useful for the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease associated with the protein, or for diagnosing and treating
 CC disorders associated with the NOVX protein, such as cancer, myelogenous

CC leukaemia, congenital neonatal autoimmune thrombocytopaenia,
 CC immunological disorders, allergy and infection, asthma, lung diseases,
 CC reproductive disorders, male and female reproductive diseases,
 CC haemangioma, deafness, liver cirrhosis, hepatitis C, gastric disorders,
 CC diabetic retinopathy, psoriasis, multiple sclerosis, atherosclerosis,
 CC hypertension, stroke and heart failure. NOV11 represents a new member of
 CC the chemokine receptor family and the gene is located on chromosome 1.
 XX
 SQ Sequence 1343 BP; 315 A; 403 C; 273 G; 352 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.52e-181 Length: 1343
 Score: 1903.00 Matches: 371
 Percent Similarity: 83.00% Conservative: 0
 Best Local Similarity: 83.00% Mismatches: 1
 Query Match: 96.75% Indels: 75
 DB: 12 Gaps: 1
 US-10-689-832-20 (1-372) x ADI79324 (1-1343)
 QY 1 MetGluHisThrHisAlaHisLeuAlaAlaAsnSerSerLeuSerTTPTrpSerProGly 20
 Db 2 ATGGAGCACACGACGACGCCACCTCGCAGCAACAGCTCGCTGTCTTGGTGTCCCCGGC 61
 QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuGly 40
 Db 62 TCGGCTCGGCTGGGTTCGTGCCGTGCTACTACAGCTCTTGTGTGCTCGGT 121
 QY 41 LeuProAlaAsnLeuThrValIleLeuSerGlnLeuValAlaArgArgGlnLys 60
 Db 122 TTACAGCAAAATATCTTGACAGTGCATCTCTCCAGCTGGTGGCAAGACAGAAG 181
 QY 61 SerSerTyrAsnTyrLeuLeuAlaAlaAspPheLeuValLeuPhePhe 80
 Db 182 TCCTCCCTACAACTATCTCTGGCAGCTCGCTGCCGACATCTTGGTCTCTTTTCATA 241
 QY 81 ValPheValAspPheLeuLeuGluAspPheLeuAsnMetGlnMetProGlnValPro 100
 Db 242 GTGTTGTGGACTCTCTTGGAGATTTCATCTTGAACATGCAGATGCCTCAGTCCCC 301
 QY 101 AspLysIleLeuValLeuGluPheSerSerIleHisThrSerIleTTPIleThrVal 120
 Db 302 GACAAAGATCATAGAAGTGTGGAATTCATCTCCATCCACACCTCCATATGGATTACTGTA 361
 QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
 Db 362 CCGTTAAACCATTTGACAGGTATATCAGTCTGCCACCCCGCTCAAGTACCACACCGTCTCA 421
 QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
 Db 422 TACCCAGCCCGCACCCCGGAAGTCAATTGTAAGTGTTTACATCACCTGCTTCTGACCCAGC 481
 QY 161 IleProTyrTyrTTPTrpProAsnIleTTPThrGluAspTyrIleSerThrSerValHis 180
 Db 482 ATCCCTTATTACTGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 541
 QY 181 HisValLeuIleTTPIleHisCysPheThrValTyrIleValProCysSerIlePhePhe 200
 Db 542 CACGTCCTCATCTGGATCCACTGCTTCACCGCTTACCTGGTGGCTGCTCCTCTCTTC 601
 QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
 Db 602 ATCTTGAACCTCAATCATTTGTGTACAGCTCAGGAGGAAGACCAATTTTCTCTCGGTGC 661
 QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
 Db 662 TACTCCAGCGGGAAGACCAACCGCCATCTTGTTCACCATTTACCTCATCTTTGCCACACTT 721
 QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
 Db 722 TGGGCCCCCGGCATCATGATTTTACACCTCTATGGGGCGCCCATCCAGAACCGC 781
 QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280

Db 782 TGGCTGGTACACATCATGTCGACATTTGCCAATCTAGCCCTTCTGAACACAGCCATC 841
Qy 281 AenPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 842 AACTTCTCTCTACTGCTTCTATCAGCAGCGGTCCGACCATGACGCCGCCAGCTC 901
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 902 AAGGCTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTACACCAATATAAATTTTCC 961
Qy 321 IleThrSerSerProTyrPheSerProAlaAsnSerHisCysIleIleValTyr 340
Db 962 ATAACAAGTAGGCCCTCGGATCTCGCCGCAAACTCACACTGCATCAAGATGCTGGTAC 1021
Qy 341 GlnTyrAspLysAsnGlyLysProIle-Lys----- 350
Db 1022 CAGTATGACAAAATGGAACCTATAAAGTATCCCCGTGATTCATAGGTGTGGCAAC 1081
Qy 350 ----- 350
Db 1082 TACTGCTCTGTCTAATCCATTTCCAGATGGGAAGGTGCCATCTATGGCTGAGCAGC 1141
Qy 350 ----- 350
Db 1142 TCTCCTTAAGAGTGTAAATCCGATTTCTCTCTCCGACAGACTGGGCAATTCTCAGACTG 1201
Qy 350 ----- 350
Db 1202 GTAGATGACAGAGATGGAAGAGAGAGAGAGATGAAGCTGTTTTTACTTATGCA 1261
Qy 351 -----SerArgAsnAspSerLysSerTyrGlnPheGluAspAlaIleG 366
Db 1262 TTTATTTCACAGAGTCGTAATGACAGCAAAAGCTCTACCAAGTTTGAAGATGCCATTGG 1321
Qy 366 yAlaCysValIleIleLeu 372
Db 1322 AGCTTGTGTCATCATCCTG 1340

RESULT 13

ID ADO56003 standard; cDNA; 1343 BP.

XX AC ADO56003;

XX 15-JUL-2004 (first entry)

XX DE DNA encoding human NOV11.

XX human; gene; ss; cancer; obesity; diabetic nephropathy;
KW acute pancreatitis; stroke; multiple sclerosis.

XX OS Homo sapiens.

XX PN US2004058862-A1.

XX PD 25-MAR-2004.

XX PP 18-SEP-2002; 2002US-00246583.

XX PR 18-SEP-2002; 2002US-00246583.

XX PA (MAJU/) MAJUMDER K.

XX PI Majumder K;

XX DR WPI; 2004-268835/25.

XX DR P-PSDB; ADO56004.

XX PT Novel NOVX polypeptides, useful for treating cancer, obesity, diabetic
PT nephropathy, acute pancreatitis, strokes and multiple sclerosis.

XX PS Disclosure; Page 28; 87pp; English.

XX The invention relates to novel isolated NOVX nucleic acids and encoded
CC polypeptides. The nucleic acids, polypeptides and antibodies raised
CC against the polypeptides are useful for preventing or treating diseases
CC associated with aberrant NOVX expression or activity e.g., cancer,
CC obesity, diabetic nephropathy, acute pancreatitis, stroke, multiple
CC sclerosis. The present sequence represents a NOVX nucleic acid of the
CC invention.

XX SQ Sequence 1343 BP; 315 A; 403 C; 273 G; 352 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8-528-181 Length: 1343
Score: 1903.00 Matches: 371
Percent Similarity: 83.00% Conservative: 0
Best Local Similarity: 83.00% Mismatches: 1
Query Match: 96.75% Indels: 75
DB: 12 Gaps: 1

US-10-689-832-20 (1-372) x ADO56003 (1-1343)

Qy 1 MetGluHisThrHisAlaHisLeuAlaAlaAsnSerSerLeuSerTyrTrpSerProGly 20
Db 2 ATGGAGCAACACGACGCCACCTCCAGCCCAACAGCTCGCTGCTTGGTGGTCCCCGGC 61
Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 62 TCGGCTCGGGCTTGGGTTTGTGCGCGTGGTCTACTACAGCTCTTGTGTGCTCGGT 121
Qy 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAlaArgGlnLys 60
Db 122 TTACAGCAAAATATCTTGACAGTGTATCTCTCCAGCTGGTGGCAAGACAGAG 181
Qy 61 SerSerTyrAsnTyrLeuLeuAlaAlaAspIleLeuValLeuPheIle 80
Db 182 TCCTCTAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTGGTCTCTTTTTCATA 241
Qy 81 ValPheValAspPheLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 242 GTGTTTGGACTCTCTGTGGAAGATTCATCTTGAACATGCAGATGCCTCAGGTCCC 301
Qy 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleThrVal 120
Db 302 GACAGATCATAGAGTGTGGAATTCATCATCCATCCACATCCATATGGATTACTGTA 361
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db 362 CCGTTAACCATTCAGAGGTATATCACTGTCTGCCACCCGCTCAAGTACCACAGGTCTCA 421
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 422 TACCCAGCCCGCACCCGGAAGTCAATTGTAAGTGTATACATCACCTGCTTCTGACCAGC 481
Qy 161 IleProTyrTyrTrpProAsnIleThrPheGluAspTyrIleSerThrSerValHis 180
Db 482 ATCCCTATTACTGTGGCCCCAACATCTGAGCTGAAGACTATACATCAGCACCTCTGTGCAT 541
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 542 CACGTCCTCATCTGGATCCACTGCTTACCCTGCTACCTGGTGGCTTCTCCATCTTCTTC 601
Qy 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
Db 602 ATCTTGAACATCAATCATTTGTACAACTCAGGAGGAGAGCAATTTTCTGCTCCGTGGC 661
Qy 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 662 TACTCCAGGGGAGAGACCCGCCATCTTGTTCACCATTTACCTCCATCTTTGCCACATT 721
Qy 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
Db 722 TGGGCCCCCGCATCATCATGATTTCTTACCACCTCTATGGGGCGCCCATCCAGAACCCG 781

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QY 261 TrpLeuValHisIleMetSerAspIleAlaAenMetLeuAlaLeuLeuAAsnThrAlaIle 280
Db 782 TGGCTGGTACATCATGTCCGACATTCGCAACATGCTAGCCCTTCTGAACACAGCCATC 841
QY 281 AenPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaAlaThrLeu 300
Db 842 AACTTCTTCTCTACTGCTTCATCAGCAAGCGGTTCCGACCATGGCAGCGCCACGCTC 901
QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAAsnHISAsnPheSer 320
Db 902 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCC 961
QY 321 IleThrSerSerProTrpIleSerProAlaAenSerHisCysIleLysMetLeuValTyr 340
Db 962 ATAACAGTAGCCCTCGATCTCGCGCAACTCACACTGCATGCATCAAGATGCTGTGTAC 1021
QY 341 GlnTyrAspLysAAsnGlyLysProIle-Lys----- 350
Db 1022 CAGTATGACAAATGGAACCTATATAAAGTATATCCCGTGATTCATAGGTGGCAAC 1081
QY 350 ----- 350
Db 1082 TACTGCCTCTGTCTAATCCATTTCCAGATGGAGGTGTCCCATCTATGGCTGAGCAGC 1141
QY 350 ----- 350
Db 1142 TCTCCTTAAGAGTGTAAATCCGATTTCTGTCTCCCGCAGACTGGGCAATTTCTAGACTG 1201
QY 350 ----- 350
Db 1202 GTAGATGAGAGAGATGGAAGAGAGAAAGGAGACATCAAGCTTGTTTTACTTATGCA 1261
QY 351 -----SerArgAAsnAspSerLysSerTyrGlnPheGluAspAlaIleG1 366
Db 1262 TTTATTTCCACAGACTCGTAAATGACAGCAAAAGCTCTACCAGTTTGAAGATGCCATTGG 1321
QY 366 yAlaCysValIleIleLeu 372
Db 1322 AGCTTGTGTCATCATCCTG 1340

RESULT 14
AD028955
ID AD028955 standard; cDNA; 2273 BP.
XX
AC AD028955;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human novel GPCR PGR3 polynucleotide, SEQ ID NO:54.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cystostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; anti allergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
XX WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.
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XX 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
DR P-PSDB; ADO28954.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 13; SEQ ID NO 54; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2273 BP; 503 A; 691 C; 549 G; 530 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,76e-180 Length: 2273
Score: 1903.00 Matches: 271
Percent Similarity: 83.00% Conservative: 0
Best Local Similarity: 83.00% Mismatches: 1
Query Match: 96.75% Indels: 75
DB: 12 Gaps: 1

US-10-689-832-20 (1-372) x ADO28955 (1-2273)
QY 1 MetGluHisThrHisAlaHisLeuAlaAAsnSerSerLeuSerTyrTrpSerProGly 20
Db 453 ATGGAGCACACGACGCGCCACCTCGACGCCAACAGCTCGTGTCTGTGGTGTCCCGCGC 512
QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 513 TCGGCCTCGCGCTTGGGTTTCGTGCCCTGTCTACTACAGCCTCTTCTGTGCTCGCT 572
QY 41 LeuProAlaAAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAArgGlnLys 60
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Db 573 TTACCAACAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCGAAGACAGAG 632
Qy 61 SerSerTyrAenTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
Db 633 TCCTCTTACAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTGGTCTCTTTTCATA 692
Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 693 GTGTTTGTGGACTCTCTGTGGAGATTTTCATCTTGAACATGACAGATGCCCTCAGGTCCCG 752
Qy 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
Db 753 GACAGATCATAGAGTGTGGAAATCTCATCTCATCACCTCCATATGATTAATCTGTA 812
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db 813 CCGTTAACCACTTACAGGTATATCACTGTCTGCCACCCGCTCAAGTACACACGGTCTCA 872
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 873 TACCCAGCCGCAACCCGGAAGTCATTGTAAGTGTTTTACATCACCTGCTTCTCGACAGC 932
Qy 161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrValHis 180
Db 933 ATCCCTTATCTACTGGTGGCCCAACATCTGACCTGAAGACTTACATCAGCACCTCTGTGCAT 992
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 993 CAGTCTCTCATCTGGATCCACTGCTTCCAGCTTACTTGGTGGCTTCCATCTCTTC 1052
Qy 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
Db 1053 ATCTTGAACCTCAATCTATGTGTACAAGCTCAGGAGGAAGCAATTTTGTCTCTCCGTGGC 1112
Qy 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 1113 TACTCCAGGGGAAGACCCGCGCATCTGTTCACCATTACTTCCATCTTTCGACACAT 1172
Qy 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
Db 1173 TGGGCCCCCGCATCATCATGATCTTTTACCACCTCTATGGGGCGCCATCCAGAACCGC 1232
Qy 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 1233 TGGCTGGTACACATCATCTCGACATTTGCCAATGTCATAGCCCTTCTGAACACAGCCATC 1292
Qy 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 1293 AACTTCTTCTCTACTGCTTTCATCAGCAAGCGGTTCGACCATGGCGCCGCGCCAGCTC 1352
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 1353 AAGGCTTTCTTCAAGTCCGCAAGCAACCTGTACAGTTCTACACCAATCATTAATCTTTC 1412
Qy 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 1413 ATAACAAGTAGCCCTCGATCTCGCGCAAACTCACACTGCATCAAGATGCTGGGTGATC 1472
Qy 341 GlnTyrAspLysAsnGlyLysProIle-Lys----- 350
Db 1473 CAGTATGACAAAAATGGAAAAACCTATAAAAGTATCCCGTGATTCCTATAGTGTGGCAAC 1532
Qy 350 ----- 350
Db 1533 TACTGCCTCTGTCTAATCATTTTCCAGATGGGAGGTGCCATCTATGGGTGAGCAGC 1592
Qy 350 ----- 350
Db 1593 TCTCCTTAAGAGTGCTAATCCGATTTCTGCTCTCCGCGAGACTGGGCAATTTCTCAGACTG 1652
Qy 350 ----- 350
Db 1653 GTAGATGAGAGAGATGGGAAGAGAAGAGAGAGATGAAGCTTGTTTTACTTATGCA 1712

Qy 351 -----SerArgAsnAspSerLysSerTyrGlnPheGluAspAlaIleG 366
Db 1713 TTTATTTCACAGAGTCGTAATGACAGCAAAAGCTCTACCAGTTTGAAGATGCCATTGG 1772
Qy 366 yAlaCysValIleIleLeu 372
Db 1773 AGCTTGTGTGCATCATCCTG 1791
RESULT 15
AAD46858
ID AAD46858 standard; cDNA; 1526 BP.
XX
AC AAD46858;
XX
DT 27-JAN-2003 (first entry)
XX
DE Human 7TM domain receptor 65507 cDNA.
XX
KW Human; adenosine deaminase; seven transmembrane domain receptor; cancer;
KW 7TM; glycoprotease; immune disorder; IGA deficiency; allergy; arrhythmia;
KW rheumatoid arthritis; diabetes; atherosclerosis; cardiovascular disorder;
KW hypertension; ischaemic heart disease; obesity; myocardial infarction;
KW endothelial cell disorder; Grave's disease; psoriasis; brain disorder;
KW Parkinson's disease; Alzheimer's disease; haematopoietic disorder;
KW cerebral oedema; metabolic disorder; liver disorder; platelet disorder;
KW chromosome mapping; tissue typing; gene therapy; neuroprotective;
KW cytostatic; anorectic; cardiant; haemostatic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 139..1200
FT /*tag= a
FT /product= "Human 65507 protein"
FT /note= "This region is specifically claimed as SEQ ID NO:
FT 12 in claim 1 of the specification"
FT sig_peptide 139..306
FT /*tag= b
FT mat_peptide 307..1197
FT /*tag= c
FT /product= "Human mature 65507 protein"
XX
WO200274960-A2.
XX
XX 26-SEP-2002.
XX
XX 08-NOV-2001; 2001WO-US051427.
XX
XX 08-NOV-2000; 2000US-0246768P.
XX 08-NOV-2000; 2000US-0246772P.
XX 15-NOV-2000; 2000US-0249185P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Leiby KR, Kapeller-Libermann R, Glucksman M;
XX
XX WPI: 2002-759898/82.
XX P-PSDB; AAE29236.
XX
XX New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules,
XX useful for diagnosing and treating cancer, immune, cardiovascular,
XX hematopoietic, brain, pain, metabolic, liver or platelet disorders, and
XX in pharmacogenomics.
XX
XX Claim 1; Fig 17; 178pp; English.
XX
XX The present invention relates to novel 38650, 28472, 5495, 65507, 81588
XX or 14354 nucleic acid molecules which encode adenosine deaminase, glyco-
XX protease or seven transmembrane domain (7TM) receptor family members.
XX Sequences of the invention are useful in diagnosing and treating cancer
XX or aberrant cellular proliferation and/or differentiation (e.g. colon or
XX lung cancer), immune disorders (e.g. selective IGA deficiency, rheumatoid

CC arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g.,
 CC hypertension, atherosclerosis, arrhythmias, ischaemic heart disease,
 CC myocardial infarction, thrombus) including endothelial cell disorders
 CC (e.g. psoriasis, Grave's disease), haematopoietic disorders, brain
 CC disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease),
 CC pain and metabolic disorders (e.g. obesity), liver disorders or platelet
 CC disorders. They are also useful in screening assays, predictive medicine
 CC (e.g. diagnostic assays, prognostic assays, monitoring clinical trials
 CC and pharmacogenetics) and prophylactic and therapeutic methods. The
 CC nucleic acids may also be used in chromosome mapping, tissue typing and
 CC forensic biology and as surrogate markers. Sequences of the invention are
 CC also used in gene therapy. The present sequence is human 7TM domain
 CC receptor 65507 cDNA

XX
 SQ Sequence 1526 BP; 343 A; 463 C; 345 G; 374 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 2, 6e-178 Length: 1526
 Score: 1879.00 Matches: 366
 Percent Similarity: 82.33% Conservative: 2
 Best Local Similarity: 81.88% Mismatches: 4
 Query Match: 95.53% Indels: 75
 DB: 6 Gaps: 1

US-10-689-832-20 (1-372) x AAD46858 (1-1526)

QY 1 MetGluHisThrHisAlaHisLeuAlaAlaAnSerSerLeuSerTrpTrpSerProGly 20
 DB 139 ATGAGACACACGACGCCACCTCGCAGCCACAGCTCGTCTGTGGTGGTCCCGGC 198
 QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
 DB 199 TCGGCTCGGGCTGGGTTCGTGGCGGTGCTACTACGCTCTTGCAAGTGGCTCGGT 258
 QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAArgGlnLys 60
 DB 259 TTACCAGCAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAAGACAGAAG 318
 QY 61 SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
 DB 319 TCCTCTCACTATCTCTTGGCACTCGTGTGCGCAGCATCTTGGTCTCTTTTCATA 378
 QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuLeuAsnMetGlnMetProGlnValPro 100
 DB 379 GTGTTGTGGACTTCCTGTGTGAAGATTTCATCTTGAACATGCAGATGCCCTCAGTCCCC 438
 QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
 DB 439 GACAAGATCATAGAAGTGTGGAATTCATCCATCCACACCTCCATATGGATTACTGTA 498
 QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
 DB 499 CCGTTAACCATTTGACAGGTATATCGTGTGCGCACCGCTCAAGTACACACGGTCTCA 558
 QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
 DB 559 TACCAGCCCGCCCGGAAAGTCATTGTAGTGTATTACATCACCTGCTCTCTGACGAGC 618
 QY 161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
 DB 619 ATCCCTTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 678
 QY 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
 DB 679 CACGTCCTCATCTGGGTCCACTGCTTCCCGTACCGGTACCGAGGTGCCCTGCTCCATCTTCTTC 738
 QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220
 DB 739 ATCTTGAACTCAATCGTTGTGTACAGCTCAGGAGGAAGCAATTTTCGTCTGTGGC 798
 QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
 DB 799 TACTCCAGGGGAAGACCACCGCCATCTGTTCACCATTAACCTCACTCTTTGCCACTCTT 858

QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
 DB 859 TGGCCCCCGCATCATCATGATTTTACCACCTCTATGGGGCGCCCATCCAGAACGCG 918
 QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
 DB 919 TGGCTGGTACACATCATGTCCGACATTTGCCACATGCTAGCCCTTCTGAACACAGCCATC 978
 QY 281 AsnPheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrIleu 300
 DB 979 AACTTCTTCTCTACTGCTTCATCAGCAAGCGGTTCGCGACCATGGCAGCGCCACGCTC 1038
 QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
 DB 1039 AAGCTTTTCTTCAAGTCCCAAGAACCTGTACAGTTCTACACCAATCATAACTTTTTC 1098
 QY 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
 DB 1099 ATAACAAGTAGCCCTCGACTCTCGCGCAAACTCACACTGCATCAAGATGCTGTTGATAC 1158
 QY 341 GlnTyrAspLysAsnGlyLysProIle-Lys- 350
 DB 1159 CAGTATGACAAAAATGAAAAACCTATAAAGTATCCCGGTGATTCCATAGGTGGCAAC 1218
 QY 350 ----- 350
 DB 1219 TACTGCCTGTCTAAATCCATTTCCAGATGGGAAGGTGTCCCATCTCTATGCTGAGCAGC 1278
 QY 350 ----- 350
 DB 1279 TCTCCTTAAGAGTCTAATCCGATTTCTCTCTCCGACAGACTGGGCAATTTCTCAGACTG 1338
 QY 350 ----- 350
 DB 1339 GTAGATGAGAAGAGATGGAAGAGAAAGAGAGAGCATGAAGCTTGTTTTACTTATGCA 1398
 QY 351 -----SerArgAsnAspSerLysSerSerTyrGlnPheGluAspAlaIleG1 366
 DB 1399 TTTATTTTCCACAGAGTCGTAAATGACAGCAAAAGCTCTACCCAGTTTGAAAGATGCCATTGG 1458
 QY 366 YAlaCysValIleIleLeu 372
 DB 1459 AGCTTGTGTATCATCTCTG 1477

Search completed: February 12, 2005, 13:49:36
 Job time : 581 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 18:19:58 ; Search time 41 Seconds
(without alignments)
872.991 Million cell updates/sec

Title: US-10-689-832-20
Perfect score: 1967
Sequence: 1 MEHTAHLANSSLSWSFG.....NDSKSSYOFDAIGACVIL 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	242	12.3	411	2 I56444	thyrotropin-relea
2	242	12.3	412	2 S23436	thyroliberin recep
3	241	12.3	393	2 A39251	thyrotropin-releas
4	238.5	12.1	398	2 JN0708	thyrotropin-releas
5	231.5	11.8	355	2 A45177	chemokine (C-C) re
6	226	11.5	352	2 J50296	thyrotropin-releas
7	225	11.4	357	2 JCT319	probable allatosta
8	225	11.4	423	2 JCT677	allatostatin recep
9	219.5	11.2	388	2 JN0605	sonatostatin recep
10	219	11.1	384	2 A47249	brain-specific som
11	217.5	11.1	340	2 T18704	hypothetical prote
12	217.5	11.1	394	2 JCT209	gallatin receptor
13	217.5	11.1	658	2 JCR011	G protein-coupled
14	217	11.0	367	2 JCT421	opioid receptor ho
15	217	11.0	367	2 I49022	kappa opioid recep
16	217	11.0	367	2 I56520	G protein-coupled
17	214.5	10.9	595	2 JCR012	G protein-coupled
18	213.5	10.9	355	2 I49339	macrophage inflam
19	213	10.8	352	2 A45747	neuropeptide Y/pep
20	213	10.8	370	2 S43087	orphan opioid rece
21	213	10.8	384	2 JCT4629	sonatostatin recep
22	212	10.8	360	2 T23063	hypothetical prote
23	211.5	10.8	376	2 T24368	hypothetical prote
24	211.5	10.8	380	2 JCT338	kappa opioid recep
25	211.5	10.8	504	2 T29338	hypothetical prote
26	210.5	10.7	380	2 S36143	kappa opioid recep
27	209	10.6	424	2 JH0164	neurotensin recep
28	208.5	10.6	477	2 JCT913	capa receptor (CGI
29	207.5	10.5	363	2 I57940	sonatostatin recep

ALIGNMENTS

RESULT 1

I56444

thyrotropin-releasing hormone receptor - mouse

C:Species: Mus sp. (mouse)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 11-Jan-2000

C:Accession: I56444

R:Sellar, R.E.; Taylor, P.L.; Lamb, R.P.; Zabavnik, J.; Anderson, L.; Eidne, K.A.

J. Mol. Endocrinol. 10, 199-206, 1993

A:Title: Functional expression and molecular characterization of the thyrotropin-releas

A:Reference number: I56444; MUID:93249585; PMID:8387312

A:Accession: I56444

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-411 <RES>

A:Cross-references: GB:S60053; NID:g300151; PIDN:AAB26491.1; PID:g300152

C:Superfamily: adenosine receptor A1

Query Match 12.3%; Score 242; DB 2; Length 411;
Best Local Similarity 22.6%; Pred. No. 1.4e-12;
Matches 83; Conservative 71; Mismatches 125; Indels 88; Gaps 14;

Qy	19	PGSACGLGF-VPVVYVYSLLC-LGLPANILTVILSQLVARRQKSSYN-YLLALAAADIL 75
Db	16	PQVAVALEYQVTVILLVVVICGLGIVGNIMVVLVVMR--TKHMTATNCYLVS LAVADIM 73
Qy	76	VLPTIVFDLLEDFILNMQMPQVPDKI-----IEVLEPSSIHSTIWTPL 122
Db	74	VL-----VAAGLPNITDSIYGSWVYGVGCLCITYLQYLGINASSCSITAF 119
Qy	123	TIDRYIAVCHPLKHTVSYSPARTKRVIVSVVITCFLTSIPYVW-----PNIWT-EDVIS 176
Db	120	TIERYIAICHPIKAQPLCTFSRAKIIIFWA---FTSIYCMLEFFLLDLNISTYKDAIV 176
Qy	177	TSVHHVLWIHCFTVYLVPSCIFPILNSIYVYKL-----PNIWT-EDVIS 210
Db	177	ISCGYKISRNYSPIYLMDFGVYVMPMLATVLYGFIARILFLNPIPSDPKNSKTWKN 236
Qy	211	---PRKSNFRLRG-----YSTGKTTALTPTITSIPATLWAP-RIMILYHYLGAPI 257
Db	237	DSTHQNKMNLTNTTRCNFNSVSSRKQVTKMLVVVILFALLWMPYRTLVVVNSFLSPFF 296
Qy	258	QNRVLVHMSDIANMLALTAINFFLYCFISKSPRTMAAATLKAFKKCKQKQPVQFYTNH 317
Db	297	QENWFL-----FCRCIYLNSAINPVYINLMSQKFR-----AARFKLCNCKQKQKPEKAANY 348
Qy	318	NFSITSS 324
Db	349	SVALNYS 355

RESULT 2

S23436

thyroliberin receptor - rat
N:Alternate names: thyrotropin-releasing hormone receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S23436; I53279; A49168; PQ0326
R:de la Pena, P.; Delgado, L.M.; del Camino, D.; Barrios, P.
Biochem. J. 284, 891-899, 1992
A>Title: Cloning and expression of the thyrotropin-releasing hormone receptor from GH(3)
A:Reference number: S23436; MUID:92322017; PMID:1377915
A:Accession: S23436
A:Molecule type: mRNA
A:Residues: 1-412 <P>
A:Cross-references: UNIPROT:Q01717; EMBL:X64630; NID:g57394; PIDN:CAA45913.1; PID:g57395
R:Kimura, N.; Arai, K.; Sahara, Y.; Suzuki, H.; Kimura, N.
Endocrinology 134, 432-440, 1994
A>Title: Estradiol transcriptionally and posttranscriptionally up-regulates thyrotropin-
A:Reference number: I53279; MUID:94102223; PMID:8275956
A:Accession: I53279
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-412 <R>
A:Cross-references: GB:D17469; NID:g464199; PIDN:BAA04289.1; PID:g464200
R:Zhao, D.; Yang, J.; Jones, K.E.; Gerald, C.; Suzuki, Y.; Hogan, P.G.; Chin, W.W.; Tash
Endocrinology 130, 3529-3536, 1992
A>Title: Molecular cloning of a complementary deoxyribonucleic acid encoding the thyrotro
A:Reference number: A49168; MUID:92283212; PMID:1317787
A:Accession: A49168
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12, 'D', 14-290, 'K', 292-412 <ZHA>
A:Experimental source: GH cells
A>Note: sequence extracted from NCBI backbone (NCBIN:104788, NCBI:P:104795)
R:Iyama, M.; Monden, T.; Satoh, T.; Iizuka, M.; Murakami, M.; Iriuchijima, T.; Mori, M.
Biochem. Biophys. Res. Commun. 184, 367-372, 1992
A>Title: Differential regulation of thyrotropin-releasing hormone receptor mRNA levels b
A:Reference number: PQ0326; MUID:92231953; PMID:1373613
A:Accession: PQ0326
A:Molecule type: mRNA
A:Residues: 30-58, 'P', 60-222, 'T', 224-261 <YAM>
A:Experimental source: strain Wistar
A>Note: the authors translated the codon ACA for residue 88 as Ala
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; transmembrane protein
F:1-22/Domain: transmembrane #status predicted <TM1>
F:32-54/Domain: transmembrane #status predicted <TM2>
F:71-92/Domain: transmembrane #status predicted <TM3>
F:116-140/Domain: transmembrane #status predicted <TM4>
F:165-186/Domain: transmembrane #status predicted <TM5>

Query Match 12.3%; Score 242; DB 2; Length 412;
Best Local Similarity 22.6%; Pred. No. 1.4e-12;
Matches 83; Conservative 71; Mismatches 125; Indels 88; Gaps 14;

Qy 19 PGSACGLGF-VPVVVYSLLC-LGLPANILTVIILSQLVARROKSSYN-VLLALAAADIL 75
Db PQAVALEYQVVTILLVVIIICGLGIVGNIMVVLVVMR--TKHMRTPNCYLVSLAVADLM 73
Qy 76 VLFFIVFVDFLEDFILNMOMPOVPDKI-----IEVLEFSSIHSTSIWITVPL 122
Db VAAGLPNITDSIYGSWVYGVGCLCITYQLYGINASSCSITAF 119
Qy 123 TIDRYIAVCHPLKHYTVSPARTKRVISVYITCFLTSIPYYW-----PNIWT-EDVIS 176
Db TIERYIAICHPIKAQFLCTFSRAKKIIFVWA---FTSIYCMWLFLLDLNISTYKDAIV 176
Qy 177 TSVHVLWIHCFTVYLVPCSIFFILNSIIVVKL----- 210
Db ISCGYKISRNYSPYILMDFGVYVPMILATVLYGFIARILFLNPISDPKSKWKWN 236
Qy 211 ---RKSKNFRLRG-----YSTGKTTAILFTITSIFATLWAP--RIIMLYHLYGAPI 257
Db DSTHQNKNNLNTNRCFNSVTSRQVTKMLAVVILFALLWMPYRTLTVVNSFLSPFF 296

Qy 258 QNRWLHVMDSIANMLLNTAINFFLYCFISKRFRTMAAATLKAFKCKQKQPVQVYTNH 317
Db 297 QENWFL-----FCRICIYLSAINPVYINLMSQKFR-----AAPRKLCKCKQKTEKAANY 348
Qy 318 NFSITSS 324
Db 349 SVALNYS 355

RESULT 3

A39251
thyrotropin-releasing hormone receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A39251
R:Straub, R.E.; Frech, G.C.; Joho, R.H.; Gershengorn, M.C.
Proc. Natl. Acad. Sci. U.S.A. 87, 9514-9518, 1990
A>Title: Expression cloning of a cDNA encoding the mouse pituitary thyrotropin-releasing
A:Reference number: A39251; MUID:91088548; PMID:2175902
A:Accession: A39251
A:Molecule type: mRNA
A:Residues: 1-393 <STR>
A:Cross-references: UNIPROT:P21761; GB:M59811; GB:M37490; NID:g202153; PIDN:AAA40480.1;
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 12.3%; Score 241; DB 2; Length 393;
Best Local Similarity 22.1%; Pred. No. 1.6e-12;
Matches 81; Conservative 75; Mismatches 123; Indels 88; Gaps 15;

Qy 19 PGSACGLGF-VPVVVYSLLC-LGLPANILTVIILSQLVARROKSSYN-VLLALAAADIL 75
Db PQAAVALEYQVVTILLVVIIICGLGIVGNIMVVLVVMR--TKHMRTPNCYLVSLAVADLM 73
Qy 76 VLFFIVFVDFLEDFILNMOMPOVPDKI-----IEVLEFSSIHSTSIWITVPL 122
Db VAAGLPNITDSIYGSWVYGVGCLCITYQLYGINASSCSITAF 119
Qy 123 TIDRYIAVCHPLKHYTVSPARTKRVISVYITCFLTSIPYYW-----PNIWT-EDVIS 176
Db TIERYIAICHPIKAQFLCTFSRAKKIIFVWA---FTSIYCMWLFLLDLNISTYKNAV 176
Qy 177 TSVHVLWIHCFTVYLVPCSIFFILNSI---IVY----- 208
Db VSCGYKISRNYSPYILMDFGVYVPMILATVLYGFIARILFLNPISDPKSKWKWN 236
Qy 209 -KLRRKSNFRLRG-----YSTGKTTAILFTITSIFATLWAP--RIIMLYHLYGAPI 257
Db DSTHQNKNNLNTNRCFNSVTSRQVTKMLAVVILFALLWMPYRTLTVVNSFLSPFF 296
Qy 258 QNRWLHVMDSIANMLLNTAINFFLYCFISKRFRTMAAATLKAFKCKQKQPVQVYTNH 317
Db 297 QENWFL-----FCRICIYLSAINPVYINLMSQKFR-----AAPRKLCKCKQKTEKAANY 348
Qy 318 NFSITSS 324
Db 349 SVALNYS 355

RESULT 4

JN0708
thyrotropin-releasing hormone receptor - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: S40682; JN0759; S50151; S50152; I38356; JN0708
R:Matre, V.; Karlsten, H.E.; Wright, M.S.; Lundell, I.; Fjeldheim, A.K.; Gabrielsen, O.S.
Biochem. Biophys. Res. Commun. 195, 179-185, 1993
A>Title: Molecular cloning of a functional human thyrotropin-releasing hormone receptor.
A:Reference number: S40682; MUID:93371401; PMID:8395824
A:Accession: S40682
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-398 <MAT>

RESULT 6

JE0296
thyrotropin releasing hormone receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 05-Dec-1998 #sequence_revision 09-Dec-1998 #text_change 09-Jul-2004
C/Accession: JE0296
R/Cladani, H.; Nakamura, T.; Itoh, J.; Iwaasa, H.; Kanatani, A.; Borkowski, J.; Ihara, M.
Biochem. Biophys. Res. Commun. 250, 68-71, 1998
A/Title: Cloning and characterization of a new subtype of thyrotropin-releasing hormone
A/Reference number: JE0296; MUID:98407892; PMID:9735333
A/Accession: JE0296
A/Molecule type: mRNA
A/Residues: 1-352 <ITA>
A/Cross-references: UNIPROT:O88820; DBJ:AB015645; NID:G3660553; PID:BA03437.1; PID:G05343
C/Superfamily: adenosine receptor A1
F/26-48/Domain: transmembrane #status predicted <TM1>
F/58-80/Domain: transmembrane #status predicted <TM2>
F/97-118/Domain: transmembrane #status predicted <TM3>
F/142-165/Domain: transmembrane #status predicted <TM4>
F/188-209/Domain: transmembrane #status predicted <TM5>
F/252-273/Domain: transmembrane #status predicted <TM6>
F/282-304/Domain: transmembrane #status predicted <TM7>

Query Match 11.5%; Score 226; DB 2; Length 352;
Best Local Similarity 23.5%; Pred. No. 2.5e-11;
Matches 76; Conservative 61; Mismatches 104; Indels 82; Gaps 11;

Qy 31 VYSLLLC-LGLPANILTVILSOLVARRQKSSYN-YLLALAAADILVLFVFDLLE 88
Db 26 VFLVLLVCTGLIGVGNAMVLVW-LTSRDVHTPTNCVLSLADLLVL----- 72

Qy 89 DFLNMQMPQVDPKI-----IEVLEPSSHTSIWITVPLTIDRYIAVCHPLK 135
Db 73 ---LAAGLEPNVSDSLGWHWIYGRAGCLGITYFQYLGINVSFSILAFTVERVIAICHPLR 129

Qy 136 YHTVSYPARFKVIVSYIICFTLSIPYWWPNLWTDYISTSVHHVLIWIHCFTVYLV 195
Db 130 AQTVCTVARAKRIIAGIAGWVTSYCLLWFFLVLDVNRDNORLECGYKVPGLYLPYLLD 189

Qy 196 CSIEFFI---LNSIIIVYKL-----RRKSNFRLR 219
Db 190 FAVFFIGPLLVTLVLYGLIGRILFQSPLSQEAQKQPHQGSAAFGNCRAKS----- 244

Qy 220 GYSTGKTTAILFTTTSIPATLWAP-RIIMILYHLYGAPIONRWLVHMSDIANMLALNT 278
Db 245 --SKQATRLMAVVVLLFAVLWTEYRTLVLLNSFVAQFPLDPWVLL----FCRTCVYVNS 298

Qy 279 AINFFLYCFTSKRPTMAAATLK 301
Db 299 AVNPVYLSMSQKFR---AAPLK 318

RESULT 7

JC7319
Probable allatostatin receptor-2 - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
C/Accession: JC7319
R/Lenz, C.; Williamson, M.; Grimmlikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 273, 571-577, 2000
A/Title: Molecular cloning and genomic organization of a second probable allatostatin receptor
A/Reference number: JC7319
A/Accession: JC7319
A/Molecule type: mRNA
A/Residues: 1-357 <LEN>
A/Cross-references: UNIPROT:Q9NBC8; GB:AF25352
C/Comment: This receptor, belonging to the insect allatostatin neuropeptide family, which is a transmembrane glycoprotein.
C/Genetics:
A/Map position: right arm of chromosome 3, 98D-E
A/Introns: 180/3; 273/3; 326/3

C;Superfamily: endothelin receptor B
C;Keywords: extracellular protein; glycoprotein; neuropeptide; transmembrane protein

Query Match 11.4%; Score 225; DB 2; Length 357;
Best Local Similarity 24.9%; Pred. No. 3.1e-11;
Matches 87; Conservative 70; Mismatches 112; Indels 80; Gaps 18;

Qy 8 LAANSLSWSPGSCAGLGPVVPVYVSYLLCLGLPANILTVIILSQLVARROKGSNNYLL 67
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 31 LAINGTLPMI-----VGFS---FFGVIAITGGFNLLVLVV--VFNNMRSTTNLMI 77
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy 68 A-LAARDILVLFIVFDPLEDFIL-----NMQMPOVDPKILEVLEFSSIHNS 115
|||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 78 VNLAAADL--MFVILCIPTATDMYYWPYGFWCRSQY-----LIIVTAFASIIY- 128
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy 116 IWITVPLTIIDRYAVCHPLKYHTVSYPARTKRVIIVSVYTICFLTSLPY----- 163
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 129 ---LVLMSIDRFLAVHPHRSRMRTENITLIAIVTLMIIVLVVSPVAFTHDVVVDYDA 185
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy 164 -----YWPNINWTDYISTSVHHVLWIHCFTVYLPCSIFFILNLIIVKLRRK----- 213
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 186 KQNITYGMCTFTNFELGRPTYQTTFPI---SSYLLPLMIISGLYMRLMRLWRQGTGVR 242
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy 214 -SNFRLEGYSTGKTALFITITSIEATLWAP-RIMILVHLYGAPIQRWLHVMSDI-A 270
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 243 MSKEQSGRK--RVTRLVVVVVIAPASLMPVQGIILLKSL--DVIETNLTCLKVLQVTA 298
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy 271 NMLALLNTAINFFLYCFISKRFRTMAATLKAPFK---COKQPVOFYTN 316
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 299 QTLAYSSSCINPLLAFLENFR-----KAFYKAVCNSSR-YQNYTS 339
||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 8
JC7677
allatostatatin receptor - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: JC7677
F;Auerswald, L.; Birguel, N.; Gaede, G.; Kreienkamp, H.J.; Richter, D.
Biochem. Biophys. Res. Commun. 282, 904-909, 2001
A;Title: Structural, functional, and evolutionary characterization of novel members of t
A;Reference number: JC7677; MUID:21250673; PMID:11352636
A;Accession: JC7677
A;Molecule type: mRNA
A;Residues: 1-423 <AUS>
A;Cross-references: UNIPROT:Q964D4; GB:AF336364
C;Comment: This receptor, for the neuro peptide, is involved in the inhibition of juvenil
C;Genetics:

```

A:Gene: Alstr
C:Keywords: neuropeptide; transmembrane protein
F:73-94/Domain: transmembrane #status predicted <TM1>
F:105-127/Domain: transmembrane #status predicted <TM2>
F:143-164/Domain: transmembrane #status predicted <TM3>
F:165-167/Region: active element DRP
F:187-207/Domain: transmembrane #status predicted <TM4>
F:243-264/Domain: transmembrane #status predicted <TM5>
F:290-312/Domain: transmembrane #status predicted <TM6>
F:327-350/Domain: transmembrane #status predicted <TM7>

Query Match          11.4%; Score 225; DB 2; Length 423;
Best Local Similarity 23.5%; Pred. No. 3,7e-11;
Matches 88; Conservative 75; Mismatches 126; Indels 86; Gaps 17;

Qy      28  VPVYVYSLLLCLGLPANILVTIILSQLVARQKSSVNYLLA-LAAADILVLFITVF-VDF 85
Db      71  VLPL-FGLIVLVLGFGNALVVLVVA--ANQCMSTNLLLIINLAVADLL---FIVFCVPF 124
Qy      86  LLEDFILNM-QMPQVPDKITLEVLFSSIHTSIWTIPLTIDRYIAVCHPLKYHTVSYPAR 144
Db      125  TATDYVLFPFPFGDIWCKIVQYLIVVTAYASVTVLVLMSLDRLAVVHPITSMSIRTEFN 184
Qy      145  TRKVIIVSVYTICFLTSPYVWPNIMTEDYISTSVHHVLIWHIC----- 188

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Db 185 AIAAIAVTVVILLASVPVLSHGVEVTTY-SAAHTACVFLSEADINRPGYNKPVFOI 243
QY 189 ---FTYLVPCSIFFILNSIIVYKLRKSNFRLGRYSTG-----KTTAILFTI 233
Db 244 IFFATSYVPLALICGLYLWLVRL-----WRGAAPGHVSAESRRGKRVTRVVVV 296
QY 234 TSIFATLWAP-RIIMLYLHYGAPIONRWLHMSDIANMLALNTAINFFLYCFISKRF 292
Db 297 VAIFAVCFWPIQLILVLKVDKYEITNTSV--MIQIVSHVLAVMNSCVNPILYAFLSDFH 354
QY 293 RTMAAATLKAFPK---C-----QKQPVQFVTNHNFSITSPWISPAHSHCKMLVQYDGN 345
Db 355 R-----KAFKRVINCAGQAQAPGRY-----HRASTIQOQPOAN 389
QY 346 GKPIKS---RNDSSKS 357
Db 390 GRALNNECVENDNKS 404

RESULT 9
somatostatin receptor 4 - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JN0605; JN0762; A47457
R:Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A:Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A:Reference number: JN0605; MUID:93290656; PMID:8512564
A:Accession: JN0605
A:Molecule type: DNA
A:Residues: 1-388 <XU>
A:Cross-references: UNIPROT:P31391; GB:L14856; NID:G292499; PIDN:AAA36623.1; PID:G292500
R:Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A:Title: Cloning, functional expression and pharmacological characterization of a fourth
A:Reference number: JN0762; MUID:93384611; PMID:8373420
A:Accession: JN0762
A:Molecule type: DNA
A:Residues: 1-388 <YAM>
A:Cross-references: GB:D16826; NID:G693907; PIDN:BA04106.1; PID:G693908
R:Roehrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A:Title: Cloning and characterization of a fourth human somatostatin receptor.
A:Reference number: A47457; MUID:93248256; PMID:8483394
A:Accession: A47457
A:Molecule type: DNA
A:Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A:Cross-references: GB:L07833; NID:G307429; PIDN:AAA60565.1; PID:G307430
A:Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBI:P:130858)
C:Comment: This protein mediates the diverse actions of the tetradaptide somatostatin.
C:Genetics:
A:Gene: GDB:SSTR4
A:Cross-references: GDB:202662; OMIM:182454
A:Map position: 20p11.2-20p11.2
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F:47-73/Domain: transmembrane #status predicted <TM1>
F:84-109/Domain: transmembrane #status predicted <TM2>
F:121-142/Domain: transmembrane #status predicted <TM3>
F:162-184/Domain: transmembrane #status predicted <TM4>
F:208-238/Domain: transmembrane #status predicted <TM5>
F:257-284/Domain: transmembrane #status predicted <TM6>
F:291-314/Domain: transmembrane #status predicted <TM7>
F:244/Binding site: carboxylate (Asn) (covalent) #status predicted
F:119-198/Disulfide bonds: #status predicted
F:161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pr
F:327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 11.2%; Score 219.5; DB 2; Length 388;
Best Local Similarity 22.0%; Pred. No. 9.6e-11;
Matches 72; Conservative 75; Mismatches 130; Indels 51; Gaps 11;
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QY 19 PGSACGLGFVPV-VYYSLLCLGLPANILTVILSQLVARRQKSSNYLLAALADILVL 77
Db 39 PGDARAAGWVAIQCIYALVGLGNALVIFVILR-YAKMKTATNIYLLNLAVALDEL-- 95
QY 78 PFIVFVDFLLEDFIL-NMQMPQVPDKIIIEVLEFSSIHSTIWIPTITDRIYAVCHPLKY 136
Db 96 -FMLSVPFVASSAALRHPFPFGLSVLCRAVLSVDGLNMTSVFCLTVLSVDRIYVAVVHPLRA 154
QY 137 HTVSYPARTRKIVSVVITCELTSTPY-----YMWPN-TWTDYIST 177
Db 155 ATYRPSVAKLNLGVWLASLLVTLPIAFADTRPARGQAVACNLQWPHPAWAVFV-- 212
QY 178 SVHVLVIWHCFV-YLVPCSIFFILNSIIVYKLR--KSNFRLRGSTGKTTAILFTI 233
Db 213 -----VYTFLLGFLLPVLAIGLCYLLIYGVKRAVALRAGWQQRSEKKITRLVLVW 264
QY 234 TSIFATLWAPRIIMLYLHYGAPIONRWLHMSDIANMLALNTAINFFLYCFISKRF 293
Db 265 VVVFVLCWMPFVYVQLNLVVTSLD-----ATVNHVSLILSYANSCANPILYGLFLSDNFR 319
QY 294 -----TWAAATLKAFPKCKQKQPVQY 314
Db 320 RSFQVLCIRCLLEGAGABEPLDYY 347

RESULT 10
A47249
Brain-specific somatostatin receptor SSTR-4 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47249
R:Bruno, J.F.; Xu, Y.; Song, J.; Berelowitz, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 11151-11155, 1992
A:Title: Molecular cloning and functional expression of a brain-specific somatostatin r
A:Reference number: A47249; MUID:93087484; PMID:1360663
A:Accession: A47249
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-384 <BRU>
A:Cross-references: UNIPROT:P30937; GB:M95544; NID:G207072; PIDN:AAA42180.1; PID:G207073
A:Note: sequence extracted from NCBI backbone (NCBIN:119731, NCBI:P:119732)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 11.1%; Score 219; DB 2; Length 384;
Best Local Similarity 20.8%; Pred. No. 1e-10;
Matches 75; Conservative 80; Mismatches 139; Indels 66; Gaps 11;

QY 3 HTHAHLAANSLSWMSPG-----SACGLGFVPV-----YYSLLCLGLPAN 44
Db 2 NTPATPLGGEDTTWPGINASWAPDEEDAVRSDGTGTAGNVTIQCIIYALVCLVLGN 61
QY 45 ILTVILSQLVARRQKSSNYLLAALADILVIFVDFLLEDFILNMQMPQVPDKII 104
Db 62 ALVIFVILR-YAKMKTATNIYLLNLAVALDELFMLSVPFVASAAA--LRHWPFGVLCRAV 118
QY 105 EVLEFSSIHSTIWIPTITDRIYAVCHPLKYHTVSYPARTRKIVSVVITCELTSTPY- 163
Db 119 LSVDFGLNMTSVFCLTVLSVDRIYVAVVHPLRAATYRRPSVAKLNLGVWLASLLVTLPTA 178
QY 164 -----YMWPN-TWTDYISTSVHHLIWHCFV-YLVPCSIFFILNS 204
Db 179 VFADTRPARGQAVACNLHWPHPAWAVFV-----YTFLLGFLLPVLAIGLCYL 228
QY 205 IIVYKLR--KSNFRLRGSTGKTTAILFTITTSIFATLWAPRIIMLYLHYGAPIONRW 261
Db 229 LIVGKRAVALRAGWQQRSEKKITRLVLMVTVTVFLCWMFPYVYVQLNLVFTSLD--- 285
QY 262 LVHMSDIANMLALNTAINFFLYCFISKRF-----TWAAATLKAFPKCKQKQPVQY 314
Db 286 --ATVNHVSLILSYANSCANPILYGLFLSDNFRSRQVLCIRCLLETGGAABEPLDYY 343
```

RESULT 11

T18704
hypothetical protein B0334.6 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18704
R/Swinburne, J.
submitted to the EMBL Data Library, October 1995
A/Reference number: Z19009
A/Accession: T18704
A/Status: preliminary; translated from GB/EMBL/DBDJB
A/Molecule type: DNA
A/Residues: 1-340 <WIL>
A/Cross-references: UNIPROT:Q17478; EMBL:Z66519; NID:gl044812; PIDN:CAA91374.1; GSPDB:GN
A/Experimental source: clone B0334
C/Genetics:
A/Gene: CESP:B0334.6
A/Map position: 2
A/Introns: 136/1; 160/3; 307/1
C/Superfamily: *Caenorhabditis elegans* hypothetical protein B0334.6

Query Match 11.1%; Score 217.5; DB 2; Length 340;
Best Local Similarity 23.1%; Pred. No. 1.2e-10;
Matches 84; Conservative 55; Mismatches 128; Indels 97; Gaps 13;

Qy 5 HAHUAANSLSWSWSPGSACGLGFVVPVYVYSLLLCLGLPANILTVIILSQLVARQKSSYN 64
Db 31 HEHDEQISIVWMS-----NNAVLPVI-----ALIGLACNLNNAVLTSNKTARRIPSWN 80
Qy 65 YLLAARAADILVLFVIFVDFLEDFEDFLNMQMPQVDPDKIIEVLEFSSIHTSIWITVPLTI 124
Db 81 LLTALAACVDSLFLFAT-----LDVTPISIPS-----LAFSTFNHFVSRIVLYI 125
Qy 125 -----DRIYAVCHPLKYHTVSPATRKVIVSVYITCFLTSIPYYWPN 168
Db 126 RTLASTFVKSSRNIPKSKFLANQILE-----KIRHVVRHIYYR----- 164
Qy 169 IWTEDYISTSVHHVLIWHCFVTLVPCSTFFFLINSIIVYKLRKRKNFRURGYS----- 222
Db 165 --TMDYVSLFAFNVL-----PIIGLLYNSRIIFTLRRVVDSDSRKYEETKLSLD 211
Qy 223 -----TGKTTAILFTITSIPATLWAPRI-IMLVHLYGAPIONRWLVHMSDIA 270
Db 212 GLIQDHANNRTWRANAMLVFAVFMLEFCVGPQAPARILFDMYG-QYHPKAIIVVC--LS 268
Qy 271 NMLALLNTAINFLFYCYFISKRFRMTAAATLKAFK-KCKQKQVQVFTYNNHFSITSSPWISP 329
Db 269 QQLVFLNASLNFCLYCVVSKRYKRYTLMKQTLLKFLHLKEGVDPHPFQINLKTQSSSAHVTS 328
Qy 330 ANSH 333
Db 329 LEDH 332

RESULT 12

JC7209
galanin receptor - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C/Accession: JC7209
R/Lenz, C.; Sondergaard, L.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 269, 91-96, 2000
A/Title: Molecular cloning and genomic organization of a novel receptor from *Drosophila*
A/Reference number: JC7209; MUID:20160456; PMID:10694483
A/Accession: JC7209
A/Molecule type: mRNA
A/Residues: 1-394 <LEN>
A/Cross-references: UNIPROT:Q9U721; GB:AF220216
C/Comment: This receptor is a G-protein-coupled receptor and a transmembrane protein.
C/Genetics:
A/Map position: X distal end
A/Map position: FlyBase:FBgn0028961

A; Introns: 98/1; 161/2; 193/2; 243/3; 283/2; 308/3; 360/3
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

	Query Match	11.1%; Score 217.5; DB 2; Length 394;
	Best Local Similarity	25.4%; Pred. No. 1.4e-10;
	Matches	99; Conservative 68; Mismatches 136; Indels 79; Gaps 22;
Qy	2 EHT-HAFLAANSLSWSPGSACG--LGFVPVYVYYSLLLCLGLPANILTIIILSQLVARR	58
Dd	47 EHTDSDHNANDSWEYDAESVALERIVSTIVPFFGLIGPAGLGNGLVTLV--VVANQ	103
Qy	59 Q-KSSNYNLLA-LAAADILVLPIFV-VDFLEDDFILNMQPOVP-----DKILEVLFEFS	110
Dd	104 QMRSTTNLLIINLASVDLI---EVIFCPPTATDYVL----PEWPFGNVCKRFQVMIVV	156
Qy	111 SIHTSWITVPLTIDRYIAVCHPLKYHTYSVPARTKRVIVSVVITCFELTSIP-----	162
Dd	157 TCHSCVTYLVLMSFDRLAVHVPMTSMUKTERNATIALCAWITITVTAIPVALSHSVR	216
Qy	163 -YYWNPNIWTEDIYSTVHHVLIW-----IHCF-TVLYPCSIFFILNSIIYVKL----	210
Dd	217 IYQYHGNAQTACVFSTEET---IWSLVGFQVSFFLSYVAPLTLCFLYMGMLARLKWSA	273
Qy	211 -----RKSNFRLRGYSTGKTAILTITSIFATLWAP-RIMWL--YHLYGAPIQN	259
Dd	274 PGCKPSAESRKGRRV-----TRMVVVVVLAFAICWLPIHVILVLKALNDYG--G	321
Qy	260 RVLVHMDSIDANMLALLNTAINFFLCFTSKSRFTMAAATLKAFKK--COKOPVOFYTN	316
Dd	322 SHLSVIQIIISHVAAYTNSCINPILYAFUSDNR-----KAFRKVWGCGSP-PLMTN	373
Qy	317 HNFSTISSPWISPA NSHCIKML 338	
Dd	374 QQVTKITRTATNGTNS-IEML 394	

RESULT 13
JC8011
G protein-coupled neuropeptide pyrokinin-2 receptor (CG8784) - fruit fly (Drosophila)
C; Species: Drosophila melanogaster
C; Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C; Accession: JC8011
F; Rosenkilde, C.; Cazzanali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; D.
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A; Title: Molecular cloning, functional expression, and gene silencing of two Dr
A; Reference number: JC8011; PMID: 12951076
A; Accession: JC8011
A; Molecule type: mRNA
A; Residues: 1-658 <ROS>
A; Cross-references: GB:AY27898
C; Comment: This receptor is a G protein-coupled receptor and a transmembrane pr
evolution, diapause, feeding, and behavior.

A:Gene: CG8784
A:Introns: 160/1; 215/2; 259/3; 326/1; 400/3
C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane p

	Query Match	11.1%	Score 217.5;	DB 2;	Length 658;
	Best Local Similarity	25.0%	Prod. No. 2.5e-10;		
	Matches	82;	Conservative	63;	Mismatches 132;
				Indels	51;
				Gaps	14;
Qy	31	VYSLILCLGLPANILTVITLSOLVARQKSSNYLLALAAADILVLFFVFDFLEEDF	90		
Db	112	VCVALIFVAGVLNLTICVISRNPMHTATNF-YLENLAVSDLLL-----VSGIQE-	164		
Qy	91	ILNQMPQV---PDKII---EVLEFSIHTSIWITPLTIDRIANVCHPKYHTVSPAR	144		
Db	165	LYNLWYEDMYPFTDAMCIMGSVLSEMAANAATVITFTATVERVIAICHPHQHTMKSLS	224		
Qy	145	TRKVIYSVITCFLTSTPIYYWPNII--WTEDYISTSVHHVLIWIHCFTV-----YLVPCS	197		
Db	225	AIKFIFAIWLAAFLALLPAQMQFSVYQNGYSGCTMEND--FYAHVPAVSGFIFFGFGPMT	282		

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QY 301 KAFFKQKQKQVQVQYTNHNFSTSPWISPA NSHCHCKMLVYQYDKNGKPIK 350
|||||
Db 301 KAFFKQKQKQVQVYTNHNFSTSPWISPA NSHCHCKMLVYQYDKNGKPIK 350
|||||

RESULT 2

Q8TDU8 PRELIMINARY; PRT; 388 AA.
ID Q8TDU8
AC Q8TDU8
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative G-protein coupled receptor.
CN Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takasuo H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083594; BAB9307.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 388 AA; 44893 MW; D8DF1CF0CC95D9D8 CRC64;

Query Match 82.5%; Score 1623; DB 2; Length 388;

Best Local Similarity 100.0%; Pred. No. 2.4e-104;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ANILTVILSQLVARRQKSSNYLLALAAADILVLFVDFVDFLEDFILNQMPQVPDK 102
|||||
Db 78 ANILTVILSQLVARRQKSSNYLLALAAADILVLFVDFVDFLEDFILNQMPQVPDK 137
|||||
QY 103 IIEVLEFSSIHSTSWITVPLTIDRYIAVCHPLKHTVSPARTKRVIVSVVITCLTSIP 162
|||||
Db 138 IIEVLEFSSIHSTSWITVPLTIDRYIAVCHPLKHTVSPARTKRVIVSVVITCLTSIP 197
|||||
QY 163 YWPNINWTEYISTSVHVLWIHCFTVYLVPSCIFFILNSIIVYKLRRKSNFRLGYS 222
|||||
Db 198 YWPNINWTEYISTSVHVLWIHCFTVYLVPSCIFFILNSIIVYKLRRKSNFRLGYS 257
|||||
QY 223 TGKTTAILFTTISIFATLWAPRIIMILYHLYGAPIQNRWLHIMSDIANMLLNTAINF 282
|||||
Db 258 TGKTTAILFTTISIFATLWAPRIIMILYHLYGAPIQNRWLHIMSDIANMLLNTAINF 317
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QY 283 FLYCFISKRFRTMAATLKAPFKCOKQVQVQYTNHNFSTSPWISPA NSHCHCKMLVYQY 342
|||||
Db 318 FLYCFISKRFRTMAATLKAPFKCOKQVQVQYTNHNFSTSPWISPA NSHCHCKMLVYQY 377
|||||
QY 343 DRNGKPIK 350
|||||
Db 378 DRNGKPIK 385
|||||

RESULT 3

Q9BYT4
ID Q9BYT4 PRELIMINARY; PRT; 265 AA.
AC Q9BYT4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative transmembrane receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21853304; PubMed=11863363; DOI=10.1006/geno.2002.6711;
RA Ottolenghi C., Barbieri M., McElreavey K., Fellous M.;
RT "Novel paralogy relations among human chromosomes support a link
RT between the phylogeny of doublesex-related genes and the evolution of
RT sex determination.";
RL Genomics 79:333-343 (2002).
DR EMBL; AJ303165; CAC33085.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Transmembrane.
FT NON_TER 1 265
FT NON_TER 265 265
SQ SEQUENCE 265 AA; 30999 MW; 8F314368A492395B CRC64;

Query Match 67.0%; Score 1317; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.3e-83;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ANILTVILSQLVARRQKSSNYLLALAAADILVLFVDFVDFLEDFILNQMPQVPDK 102
|||||
Db 14 ANILTVILSQLVARRQKSSNYLLALAAADILVLFVDFVDFLEDFILNQMPQVPDK 73
|||||
QY 103 IIEVLEFSSIHSTSWITVPLTIDRYIAVCHPLKHTVSPARTKRVIVSVVITCLTSIP 162
|||||
Db 74 IIEVLEFSSIHSTSWITVPLTIDRYIAVCHPLKHTVSPARTKRVIVSVVITCLTSIP 133
|||||
QY 163 YWPNINWTEYISTSVHVLWIHCFTVYLVPSCIFFILNSIIVYKLRRKSNFRLGYS 222
|||||
Db 134 YWPNINWTEYISTSVHVLWIHCFTVYLVPSCIFFILNSIIVYKLRRKSNFRLGYS 193
|||||
QY 223 TGKTTAILFTTISIFATLWAPRIIMILYHLYGAPIQNRWLHIMSDIANMLLNTAINF 282
|||||
Db 194 TGKTTAILFTTISIFATLWAPRIIMILYHLYGAPIQNRWLHIMSDIANMLLNTAINF 253
|||||
QY 283 FLYCFISKRFRT 294
|||||
Db 254 FLYCFISKRFRT 265
|||||

RESULT 4
Q7T2L1 PRELIMINARY; PRT; 383 AA.
ID Q7T2L1
AC Q7T2L1
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G-protein-coupled receptor 142b (Fragment).
GN Name=GPR142b;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,
RA Schloth H.B.;
RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives.";
RL FEBS Lett. 554:381-388 (2003).
RL EMBL; AY288414; AAP72123.1; -.


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RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsami S., Aburatani H., Asai K., Akiyama Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB065914; BAC06129.1; -.
DR Genew; HGNC:20088; GPR142.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PRO0237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 1464 AA; 156507 MW; PF8C63F8353ACF7E CRC64;

Query Match 37.5%; Score 737; DB 2; Length 1464;
Best Local Similarity 46.3%; Pred. No. 1.2e-42;
Matches 133; Conservative 57; Mismatches 95; Indels 2; Gaps 2;

QY 21 SAGLGFPVYVYSLLCGLPANILTVIILSQLVARROKSSVYLLALAAADILVLPFI 80
DB 1113 SPCVAGVPIVYISVLLGLPSLLTAVALARLATRTRPSYYLLALTASDIIVVI 1172
QY 81 VFVDFLEDFILNMOPQVDPKIIIEVLEPSSIHSTIWTPLTDRIYAVCHPLKHYTVS 140
DB 1173 VFAGFLQAVLARQVQAVVRTANILEFAANHASVWIAITVDEYALCHPLHRAAS 1232
QY 141 YPARTRKIVSVYITCFLTSIPYWPNIWTSDYSTSVHHVLIWTHCFTVYLPCSPFP 200
DB 1233 SPGRTRRAIAAVLSAALLTGIPFYWLDWRDTPRTDDEVLKWAHCLTVYFPCGVFL 1292
QY 201 ILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSFATLWAPRIIMILYHLYGAPIQNR 260
DB 1293 VTNSAILIHLRRGSRGLQP-RVGSTAILLGLTTLFTLLWAPRVFVMLYHMYVAPVHRD 1351
QY 261 WLVHMSDIANMLALINTAINPFLYCFISKRRF-TMAAATLKAFKFC 306
DB 1352 WLVHLDVANNVAMLHTAANFGLICFVSKTRATVRQVIHDAYLPC 1398

RESULT 10
QYTON9 PRELIMINARY; PRT; 365 AA.
AC QYTON9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G protein-coupled receptor 142.
GN Name=Gpr142;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoglund P.J., Gloriam D.E., Lagerstrom M.C.,
RA Schioth H.B.;
RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RL PDBS Lett. 554:381-388(2003).
DR EMBL; AY288428; AAP72137.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm.1.1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

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KW Receptor.
SQ SEQUENCE 365 AA; 40758 MW; ACA8649245CDAE47 CRC64;

Query Match 36.2%; Score 713; DB 2; Length 365;
Best Local Similarity 46.8%; Pred. No. 1.6e-41;
Matches 138; Conservative 51; Mismatches 96; Indels 10; Gaps 4;

QY 21 SAGLGFPVYVYSLLCGLPANILTVIILSQLVARROKSSVYLLALAAADILVLPFI 80
DB 64 SPCVAGIPIVYISVLLSGLP-----VALARLAARTKPSYHYLLALTASDIVTQVII 117
QY 81 VFVDFLEDFILNMOPQVDPKIIIEVLEPSSIHSTIWTPLTDRIYAVCHPLKHYTVS 140
DB 118 VFVDFLQAVLARQVQAVVRTANILEFAANHASVWIAVFTVDYRNALCRPLHRAYS 177
QY 141 YPARTRKIVSVYITCFLTSIPYWPNIWTSDYSTSVHHVLIWTHCFTVYLPCSPFP 200
DB 178 SPGRTRRAIAAVIGVTLTGIPFYWLDWRDTPSTMDKLLKWAHCLIVTFPCNVFL 237
QY 201 ILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSFATLWAPRIIMILYHLYGAPIQNR 260
DB 238 VTNSAILIHLRRKRGQGLRPL-VSKSTAILLGLTSLFALLWAPRIIVMLYHLYVAPVHRD 296
QY 261 WLVHMSDIANMLALINTAINPFLYCFISKRRF-TMAAATLKAFKFC--OKQPVQ 312
DB 297 WRVHLALDIANMLANLNTENVNGLYCFISKTRATVRQVICDVMACALKSQPKQ 351

RESULT 11
QYTON9 PRELIMINARY; PRT; 54 AA.
AC QYTON9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor PGR3 (Fragment).
GN Name=Gpr139;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
RA Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
RA Bergmann J.B., Gaitanaris G.A.;
RT "The G protein-coupled receptor repertoires of human and mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).
DR EMBL; AY255548; AAO85060.1; -.
DR MGD; MGI:2685341; Gpr139.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 54
SQ SEQUENCE 54 AA; 6082 MW; 5B7B44A1408F8FDD CRC64;

Query Match 13.3%; Score 262; DB 2; Length 54;
Best Local Similarity 94.4%; Pred. No. 4.4e-11;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 226 TTAIFTTTSIPATLWAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTA 279
DB 1 TTAIFTTTSIPATLWAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTA 54

RESULT 12
QYTON9 PRELIMINARY; PRT; 394 AA.
AC QYTON9;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```


QY 133 PLKHYTVSPARTKRVISVYITCFLTSIPYYW-----PNIWT-EDYISTSVHVLWI 186
 DB 130 PIKAQPLCTFSRAKKIIIFVMA---FTSIYCLMFLDLNISTYKDALVWSGKYISRN 186
 QY 187 HCFTVYLPCSPFFILNSIIVKL-----RRKSN----- 215
 DB 187 YSPYILMDFGVYVPMILATVYGFIAIILFLNIPDPKENSWMKNDSTHQNKNLN 246
 QY 216 -----FRLRGYSTGKTTAILFTITSIPATLWAP-RIIMILYHLYGAPIQNRWLHVHMS 267
 DB 247 SKTSNRYFNSTVSSRKQVTKLAVVILFALLWMPVTLVNVNLSLSPFQENWELL--- 303
 QY 268 DIANMLALLNTAINPFLYCFISKRPRTMAAATLKAFKCKQKOPQVYTNHNSITSS 324
 DB 304 -FCRICIYLSAINPVIYNLSQKR-----AAFRKLCNCKQKPEKPNYSVALSYS 355

RESULT 14

ID TRFR SHEEP STANDARD; PRT; 398 AA.
 AC Q28596;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyrotropin-releasing hormone receptor (TRH-R) (Thyroliberin receptor).
 GN Name=TRHR;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=97200775; PubMed=9048604; DOI=10.1210/en.138.3.1019;
 RA Bockmann J., Boeckers T.M., Winter C., Wittkowski W., Winterhoff H.,
 RA Deufel T., Kreutz M.R.;
 RT "Thyrotropin expression in hypophyseal pars tuberalis-specific cells is 3,5',-triiodothyronine, thyrotropin-releasing hormone, and pit-1 independent.";
 RT Endocrinology 138:1019-1028 (1997).
 RL -!- FUNCTION: Receptor for thyrotropin-releasing hormone. This receptor is mediated by G proteins which activate a phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL; X95285; CAA64606.1; -;
 DR InterPro; IPR00276; GPCR Rhodopsin.
 DR InterPro; IPR009144; ThyrotropinRHR.
 DR InterPro; IPR002120; Trlhrm_receptor.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSIN.
 DR PRINTS; PR01846; TRHRFAMILY.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 28 Extracellular (Potential).
 FT TRANSMEM 29 51 1 (Potential).
 FT DOMAIN 52 61 Cytoplasmic (Potential).
 FT TRANSMEM 62 83 2 (Potential).
 FT DOMAIN 84 99 Extracellular (Potential).
 FT TRANSMEM 100 121 3 (Potential).
 FT DOMAIN 122 144 Cytoplasmic (Potential).

FT TRANSMEM 145 168 4 (Potential).
 FT DOMAIN 169 193 Extracellular (Potential).
 FT TRANSMEM 194 215 5 (Potential).
 FT DOMAIN 216 266 Cytoplasmic (Potential).
 FT TRANSMEM 267 288 6 (Potential).
 FT DOMAIN 289 296 Extracellular (Potential).
 FT TRANSMEM 297 319 7 (Potential).
 FT DOMAIN 320 398 Cytoplasmic (Potential).
 FT DISULFID 98 179 By similarity.
 FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 398 AA; 45088 MW; 375A311D3DD2A61A CRC64;
 Query Match 12.7%; Score 249.5; DB 1; Length 398;
 Best Local Similarity 23.2%; Pred. No. 1.9e-09;
 Matches 83; Conservative 68; Mismatches 119; Indels 87; Gaps 13;
 QY 28 VPVYVYLLC-LGLPANILTVIILSQLVARQKSSYN-YLLALAAADILVFFVDF 85
 DB 26 VVTILLVLIICGLGIVGNIMVVLVVMR--TKHMTPTNCYLVSLAVADLMVL----- 75
 QY 86 LLEDFILNMQMPQVDDKI-----LEVLFPSSIHTSIWITVPLTIDRYIACH 132
 DB 76 -----VAAGLPNITDSIYGSWYGVGCLCTIYQYLGINASSCSITAFIERVIAICH 129
 QY 133 PLKHVTVSPARTKRVISVYITCFLTSIPYYW-----PNIWT-EDYISTSVHVLWI 186
 DB 130 PIKAQPLCTFSRAKKIIIFVMA---FTSIYCLMFLDLNISTYKDALVWSGKYISRN 186
 QY 187 HCFTVYLPCSPFFILNSIIVKL-----RRKSN----- 215
 DB 187 YSPYILMDFGVYVPMILATVYGFIAIILFLNIPDPKENSWMKNDSTHQNKNLN 246
 QY 216 -----FRLRGYSTGKTTAILFTITSIPATLWAP-RIIMILYHLYGAPIQNRWLHVHMS 267
 DB 247 SKTSNRYFNSTVSSRKQVTKLAVVILFALLWMPVTLVNVNLSLSPFQENWELL--- 303
 QY 268 DIANMLALLNTAINPFLYCFISKRPRTMAAATLKAFKCKQKOPQVYTNHNSITSS 324
 DB 304 -FCRICIYLSAINPVIYNLSQKR-----AAFRKLCNCKQKPEKPNYSVALSYS 355

RESULT 15

QY7PYB7
 ID Q7PYB7 PRELIMINARY; PRT; 440 AA.
 AC Q7PYB7;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE AGCP12601.
 GN Name=agCGS3608; ORFName=ENSANGG00000018385;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL; AA0801008987; EAA01756.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSIN.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL2; 1.
 SQ SEQUENCE 440 AA; 50079 MW; 959A62F3B6ABC95 CRC64;

	Query Match	12.7%; Score 249.5; DB 2; Length 440;
	Best Local Similarity	23.3%; Pred. No. 2e-09;
	Matches	69; Conservative 67; Mismatches 115; Indels 45; Gaps 8;
Qy	31 VYVSLLCGLGPANILTVIIISOLVARQRSSNYKLL-ALAAADILVLFFVFVDLFLED 89	: : : : : : : : : : : : : : : : : : : : :
Dd	35 VMNMIVALIGLIGNIFSMVILSR---PQMRSINYYLLIGLARCDTIVILTSVLFIGLCAI 91	: : : : : : : : : : : : : : : : : : : : :
Qy	90 F-----ILNQMPQPDPDKI---IEVLEFSSIHTSWITVPLTIDRVIAVCHEPLKVHVTYSYP 142	: : : : : : : : : : : : : : : : : : : : :
Dd	92 YPHGTGYLYHYHQIFPKLSLVVYPLAMIAQTASVILTUTFLERYAVACHPELRALACTY 151	: : : : : : : : : : : : : : : : : : : : :
Qy	143 ARTKKVIVSVVYTICFLTSPITYWPNPI-----WTEDYISTSVHH 181	: : : : : : : : : : : : : : : : : : : : :
Dd	152 GRARLYVVGVILVFSILYNLPFWNEVTLISSHPDGTGLTYCVKASDMRTNETYIKVHIH- 210	: : : : : : : : : : : : : : : : : : : : :
Qy	182 VLIWHCFVTYVLPVCSIFFFLNSIIYVKLRKSNFRLRGYSTGK----TTAILFTITSIF 237	: : : : : : : : : : : : : : : : : : : : :
Dd	211 ---WLVMIFVYVFLPFSLISFFNLMIYRQVRANKERQRLSRSEKRKEIGLATMLCVCVIVF 267	: : : : : : : : : : : : : : : : : : : : :
Qy	238 ATLWAPRIIMLLYHLYGAPIQRNVLVHMDSIANMALLNTAINPFLCYFCISKPR 293	: : : : : : : : : : : : : : : : : : : : :
Dd	268 LLCNLPMMMINIVEAFYSVI-----IEMVKVSNLLVTINSNVNFVIIYFGEKKF 318	: : : : : : : : : : : : : : : : : : : : :

Search completed: February 8, 2005, 18:28:26
Job time : 182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 18:20:18 ; Search time 129 Seconds
(without alignments)
939.235 Million cell updates/sec

Title: US-10-689-832-20

Perfect score: 1967

Sequence: 1 MEHTAHLANGLSWSPG.....NDSKSYQDAIGACVIL 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1967	100.0	372	10	US-09-813-432-20 Sequence 20, Appl
2	1967	100.0	372	14	US-10-219-834-19 Sequence 19, Appl
3	1967	100.0	372	14	US-10-314-076-2 Sequence 2, Appl
4	1967	100.0	372	15	US-10-174-364-20 Sequence 20, Appl
5	1967	100.0	372	15	US-10-333-946-6 Sequence 6, Appl
6	1967	100.0	372	15	US-10-246-583-20 Sequence 20, Appl
7	1967	100.0	372	16	US-10-689-832-20 Sequence 4, Appl
8	1939.5	98.6	369	14	US-10-314-076-4 Sequence 40, Appl
9	1857	94.4	350	10	US-09-813-432-60 Sequence 60, Appl
10	1857	94.4	350	15	US-10-174-364-60 Sequence 60, Appl
11	1857	94.4	350	15	US-10-246-583-60 Sequence 60, Appl
12	1857	94.4	350	16	US-10-689-832-60 Sequence 60, Appl
13	1857	94.4	353	9	US-09-995-225-16 Sequence 16, Appl

14 1857 94.4 353 10 US-09-995-225-16 Sequence 16, Appl
15 1857 94.4 353 14 US-10-094-417-2 Sequence 2, Appl
16 1857 94.4 353 15 US-10-296-294A-5 Sequence 5, Appl
17 1857 94.4 353 15 US-10-450-590-2 Sequence 2, Appl
18 1857 94.4 353 16 US-10-779-104-2 Sequence 2, Appl
19 1853 94.2 350 10 US-09-813-432-59 Sequence 59, Appl
20 1853 94.2 350 15 US-10-174-364-59 Sequence 59, Appl
21 1853 94.2 350 15 US-10-246-583-59 Sequence 59, Appl
22 1853 94.2 350 16 US-10-689-832-59 Sequence 22, Appl
23 1853 94.2 353 10 US-09-813-432-22 Sequence 22, Appl
24 1853 94.2 353 15 US-10-174-364-22 Sequence 22, Appl
25 1853 94.2 353 15 US-10-246-583-22 Sequence 22, Appl
26 1853 94.2 353 16 US-10-689-832-22 Sequence 22, Appl
27 1829 93.0 353 14 US-10-012-140-11 Sequence 11, Appl
28 1741 88.5 345 14 US-10-094-417-20 Sequence 20, Appl
29 1628 82.8 318 15 US-10-174-364-85 Sequence 85, Appl
30 1628 82.8 318 15 US-10-246-583-85 Sequence 85, Appl
31 1623 82.5 333 14 US-10-079-384-26 Sequence 26, Appl
32 1623 82.5 343 15 US-10-450-590-8 Sequence 8, Appl
33 1623 82.5 356 15 US-10-450-590-7 Sequence 7, Appl
34 1623 82.5 385 15 US-10-343-650A-22 Sequence 22, Appl
35 1471 74.8 287 10 US-09-791-932-66 Sequence 66, Appl
36 1426 72.5 272 10 US-09-813-432-57 Sequence 57, Appl
37 1426 72.5 272 10 US-09-813-432-58 Sequence 58, Appl
38 1426 72.5 272 15 US-10-174-364-57 Sequence 57, Appl
39 1426 72.5 272 15 US-10-246-583-57 Sequence 57, Appl
40 1426 72.5 272 16 US-10-689-832-57 Sequence 57, Appl
41 1426 72.5 272 16 US-10-689-832-58 Sequence 58, Appl
42 1317 67.0 265 14 US-10-225-567A-587 Sequence 587, Appl
43 1317 67.0 265 14 US-10-314-076-14 Sequence 14, Appl
44 912.5 46.4 313 10 US-09-791-932-63 Sequence 63, Appl
45 742 37.7 348 15 US-10-328-916-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-813-432-20
; Sequence 20, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1 Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843

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; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-432-20

Query Match      100.0%; Score 1967; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSSLSWSPGSACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60
DB 1 MEHTHAHLAANSSLSWSPGSACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60

QY 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLEFSSHTSIWTV 120
DB 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLEFSSHTSIWTV 120

QY 121 PLTIDRYIAVCHPLKHTVSYSPARTKRVIVSVYITCFLTSIPYYWPNWTEYISTSVH 180
DB 121 PLTIDRYIAVCHPLKHTVSYSPARTKRVIVSVYITCFLTSIPYYWPNWTEYISTSVH 180

QY 181 HVLWIHCFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
DB 181 HVLWIHCFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALINTAINPFLYCFISKRFTWAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALINTAINPFLYCFISKRFTWAAATL 300

QY 301 KAFFKCKQKQVQFYTNHNFSSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
DB 301 KAFFKCKQKQVQFYTNHNFSSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360

QY 361 FEDAIGACVIL 372
DB 361 FEDAIGACVIL 372

RESULT 2
US-10-219-834-19
; Sequence 19, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219,834
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313,658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-19

Query Match      100.0%; Score 1967; DB 14; Length 372;
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Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEHTHAHLAANSSLSWSPGSACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60

QY 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLEFSSHTSIWTV 120
DB 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLEFSSHTSIWTV 120

QY 121 PLTIDRYIAVCHPLKHTVSYSPARTKRVIVSVYITCFLTSIPYYWPNWTEYISTSVH 180
DB 121 PLTIDRYIAVCHPLKHTVSYSPARTKRVIVSVYITCFLTSIPYYWPNWTEYISTSVH 180

QY 181 HVLWIHCFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
DB 181 HVLWIHCFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALINTAINPFLYCFISKRFTWAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALINTAINPFLYCFISKRFTWAAATL 300

QY 301 KAFFKCKQKQVQFYTNHNFSSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
DB 301 KAFFKCKQKQVQFYTNHNFSSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360

QY 361 FEDAIGACVIL 372
DB 361 FEDAIGACVIL 372

RESULT 3
US-10-314-076-2
; Sequence 2, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY34, AND VARIANTS THEREOF
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338,371
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-076-2

Query Match      100.0%; Score 1967; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSSLSWSPGSACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60
DB 1 MEHTHAHLAANSSLSWSPGSACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60

QY 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLEFSSHTSIWTV 120
DB 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVDPDKIEVLEFSSHTSIWTV 120

QY 121 PLTIDRYIAVCHPLKHTVSYSPARTKRVIVSVYITCFLTSIPYYWPNWTEYISTSVH 180
DB 121 PLTIDRYIAVCHPLKHTVSYSPARTKRVIVSVYITCFLTSIPYYWPNWTEYISTSVH 180

QY 181 HVLWIHCFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
DB 181 HVLWIHCFTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
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DB 241 WAPRIIMILYHLYGAPIONRWLHMSDIANMLALNTAINFFLYCFISKRFRTMAAATL 300
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DB 301 KAFFKCKQKQVQFYTHNFSSPWI SPANSHCIKMLVYQYDKNGKPKIKSRNDSKSSYQ 360
QY 361 FEDAIGACVIL 372
DB 361 FEDAIGACVIL 372

RESULT 4
US-10-174-364-20
; Sequence 20, Application US/10174364
; Publication No. US20030216308A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729C1P2
; CURRENT APPLICATION NUMBER: US/10/174,364
; CURRENT FILING DATE: 2002-06-17
; PRIOR FILING DATE: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-364-20

Query Match 100.0%; Score 1967; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSLSWSPGACGLGFPVVPVYSLLLCLGLPANILTVILSOLVARROK 60
DB 1 MEHTHAHLAANSLSWSPGACGLGFPVVPVYSLLLCLGLPANILTVILSOLVARROK 60
QY 61 SSVNYLLAALAAADILVLFVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
DB 61 SSVNYLLAALAAADILVLFVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
QY 121 PLTIDRYIAVCHPKYHTVSPARTKVIIVSVVITCFLTSIPYWWPNWTEYISTSVH 180
DB 121 PLTIDRYIAVCHPKYHTVSPARTKVIIVSVVITCFLTSIPYWWPNWTEYISTSVH 180
QY 181 HVLIIWHCFVTVLPVCSIPFILNSIIVYKLRKSNFRLRGYSTGKTKTALLFTTISIPATL 240
DB 181 HVLIIWHCFVTVLPVCSIPFILNSIIVYKLRKSNFRLRGYSTGKTKTALLFTTISIPATL 240
QY 241 WAPRIIMILYHLYGAPIONRWLHMSDIANMLALNTAINFFLYCFISKRFRTMAAATL 300
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DB 241 WAPRIIMILYHLYGAPIONRWLHMSDIANMLALNTAINFFLYCFISKRFRTMAAATL 300
QY 301 KAFFKCKQKQVQFYTHNFSSPWI SPANSHCIKMLVYQYDKNGKPKIKSRNDSKSSYQ 360
DB 301 KAFFKCKQKQVQFYTHNFSSPWI SPANSHCIKMLVYQYDKNGKPKIKSRNDSKSSYQ 360
QY 361 FEDAIGACVIL 372
DB 361 FEDAIGACVIL 372

RESULT 5
US-10-333-946-6
; Sequence 6, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
; APPLICANT: HAPALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474767CD1
US-10-333-946-6

Query Match 100.0%; Score 1967; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEHTHAHLAANSLSWSPGACGLGFPVVPVYSLLLCLGLPANILTVILSOLVARROK 60
QY 61 SSVNYLLAALAAADILVLFVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
DB 61 SSVNYLLAALAAADILVLFVFDLLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
QY 121 PLTIDRYIAVCHPKYHTVSPARTKVIIVSVVITCFLTSIPYWWPNWTEYISTSVH 180
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Db 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVVITCFLTSIPYYWPNWTEDYSTSVH 180
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Db 181 HVLIIWHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRFRTWAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRFRTWAAATL 300
QY 301 KAFFKCKQKQPVQFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFFKCKQKQPVQFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
QY 361 FEDAIGACVUIL 372
Db 361 FEDAIGACVUIL 372

RESULT 6

US-10-246-583-20
; Sequence 20, Application US/10246583
; Publication No. US20040058862A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-20

Query Match 100.0%; Score 1967; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEHTHAHLAANSLSWSPGSCAGLGFPVYVYSLLLCGLGPANILTVIILSQLVARROK 60
QY 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLFFSSHTSTWTV 120
Db 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLFFSSHTSTWTV 120
QY 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVVITCFLTSIPYYWPNWTEDYSTSVH 180
Db 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVVITCFLTSIPYYWPNWTEDYSTSVH 180

QY 181 HVLIIWHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
Db 181 HVLIIWHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRFRTWAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRFRTWAAATL 300
QY 301 KAFFKCKQKQPVQFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFFKCKQKQPVQFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
QY 361 FEDAIGACVUIL 372
Db 361 FEDAIGACVUIL 372

RESULT 7

US-10-689-832-20
; Sequence 20, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729DIV1
; CURRENT APPLICATION NUMBER: US/10/689,832
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-832-20

Query Match 100.0%; Score 1967; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSLSWSPGSCAGLGFPVYVYSLLLCGLGPANILTVIILSQLVARROK 60
Db 1 MEHTHAHLAANSLSWSPGSCAGLGFPVYVYSLLLCGLGPANILTVIILSQLVARROK 60
QY 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLFFSSHTSTWTV 120
Db 61 SSYNVLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLFFSSHTSTWTV 120
QY 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVVITCFLTSIPYYWPNWTEDYSTSVH 180
Db 121 PLTIDRYIAVCHPLKHYTVSPARTRKIVSVVITCFLTSIPYYWPNWTEDYSTSVH 180

QY 181 HVLIIHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
Db 181 HVLIIHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFELYCFISKRPRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFELYCFISKRPRTMAAATL 300
QY 301 KAFFKCKQKQPVQYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFFKCKQKQPVQYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
QY 361 FEDAIGACVIL 372
Db 361 FEDAIGACVIL 372

RESULT 8

US-10-314-076-4
; Sequence 4, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV34, AND VARIANTS A
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338,371
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-076-4

Query Match 98.6%; Score 1939.5; DB 14; Length 369;
Best Local Similarity 99.2%; Pred. No. 1.1e-170;
Matches 369; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
Db 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
QY 61 SSYNYLLAALAAADILVLPFIIVFDLLEDFILNMOMQVDPDKIIEVLEFSSHTSIWTV 120
Db 61 SSYNYLLAALAAADILVLPFIIVFDLLEDFILNMOMQVDPDKIIEVLEFSSHTSIWTV 120
QY 121 PLTIDRYIACHPLKHTVSYPARTKVIIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180
Db 121 PLTIDRYIACHPLKHTVSYPARTKVIIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180
QY 181 HVLIIHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
Db 181 HVLIIHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFELYCFISKRPRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFELYCFISKRPRTMAAATL 300
QY 301 KAFFKCKQKQPVQYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFFKCKQKQPVQYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 357
QY 361 FEDAIGACVIL 372
Db 358 FEDAIGACVIL 369

RESULT 9

US-09-813-432-60

; Sequence 60, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-432-60

Query Match 94.4%; Score 1857; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.4e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
Db 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARROK 60
QY 61 SSYNYLLAALAAADILVLPFIIVFDLLEDFILNMOMQVDPDKIIEVLEFSSHTSIWTV 120
Db 61 SSYNYLLAALAAADILVLPFIIVFDLLEDFILNMOMQVDPDKIIEVLEFSSHTSIWTV 120
QY 121 PLTIDRYIACHPLKHTVSYPARTKVIIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180
Db 121 PLTIDRYIACHPLKHTVSYPARTKVIIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180
QY 181 HVLIIHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
Db 181 HVLIIHCFVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFELYCFISKRPRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFELYCFISKRPRTMAAATL 300
QY 301 KAFFKCKQKQPVQYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350
Db 301 KAFFKCKQKQPVQYTNHNFSTSSPWISPANSHCIKMLVYQYDKNGKPIK 350

RESULT 10

US-10-174-364-60
; Sequence 60, Application US/10174364
; Publication No. US20030216308A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2
; CURRENT APPLICATION NUMBER: US/10/174,364
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-364-60

Query Match 94.4%; Score 1857; DB 15; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.4e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60
Db 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60

QY 61 SSNYLLALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLEFSSHTSIWTV 120
Db 61 SSNYLLALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLEFSSHTSIWTV 120

QY 121 PLTIDRYIAVCHPLKHYTVSPARTKVIIVSVYITCFLTSIPYYWPNWIEDYISTSVH 180
Db 121 PLTIDRYIAVCHPLKHYTVSPARTKVIIVSVYITCFLTSIPYYWPNWIEDYISTSVH 180

QY 181 HVLWIHCFVTYLVPCSIFFILNSIIVYKLARKSNFRLRGYSTGKTTALTITTSIFATL 240
Db 181 HVLWIHCFVTYLVPCSIFFILNSIIVYKLARKSNFRLRGYSTGKTTALTITTSIFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300

QY 301 KAFFKCKQKQVQFYTNHNSITSSPWSIPANSHCIKMLVYQDKNGKPK 350
Db 301 KAFFKCKQKQVQFYTNHNSITSSPWSIPANSHCIKMLVYQDKNGKPK 350

RESULT 11
US-10-246-583-60
; Sequence 60, Application US/10246583
; Publication No. US2004005862A1
; GENERAL INFORMATION:
; APPLICANT: Majumder

; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-60

Query Match 94.4%; Score 1857; DB 15; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.4e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60
Db 1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLCGLPANILTVIILSQLVARROK 60

QY 61 SSNYLLALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLEFSSHTSIWTV 120
Db 61 SSNYLLALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIEVLEFSSHTSIWTV 120

QY 121 PLTIDRYIAVCHPLKHYTVSPARTKVIIVSVYITCFLTSIPYYWPNWIEDYISTSVH 180
Db 121 PLTIDRYIAVCHPLKHYTVSPARTKVIIVSVYITCFLTSIPYYWPNWIEDYISTSVH 180

QY 181 HVLWIHCFVTYLVPCSIFFILNSIIVYKLARKSNFRLRGYSTGKTTALTITTSIFATL 240
Db 181 HVLWIHCFVTYLVPCSIFFILNSIIVYKLARKSNFRLRGYSTGKTTALTITTSIFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300

QY 301 KAFFKCKQKQVQFYTNHNSITSSPWSIPANSHCIKMLVYQDKNGKPK 350
Db 301 KAFFKCKQKQVQFYTNHNSITSSPWSIPANSHCIKMLVYQDKNGKPK 350

RESULT 12
US-10-689-832-60
; Sequence 60, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729DIV1
; CURRENT APPLICATION NUMBER: US/10/689,832
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/813,432


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; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-689-832-60

Query Match          94.4%; Score 1857; DB 16; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.4e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARRQK 60
DB 1 MEHTHAHAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARRQK 60

QY 61 SSNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIEIIEVLEFSSIHSTWITV 120
DB 61 SSNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIEIIEVLEFSSIHSTWITV 120

QY 121 PLTIDRYIAVCHPLKHTVSYPARTKRVIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180
DB 121 PLTIDRYIAVCHPLKHTVSYPARTKRVIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180

QY 181 HVLWIHCFTVYLVPSCIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
DB 181 HVLWIHCFTVYLVPSCIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300

QY 301 KAFFKCKQKQVQFYTNHNSITSSPWISPANSHCIKMLVYQYDKNGKPIK 350
DB 301 KAFFKCKQKQVQFYTNHNSITSSPWISPANSHCIKMLVYQYDKNGKPIK 350

RESULT 13
US-09-995-225-16
; Sequence 16, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
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; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1e1 Sequence
; US-09-995-225-16

Query Match          94.4%; Score 1857; DB 9; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.4e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARRQK 60
DB 1 MEHTHAHAANSSLSWSPGACGLGFVPVYVYSLLLCLGLPANILTVIILSOLVARRQK 60

QY 61 SSNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIEIIEVLEFSSIHSTWITV 120
DB 61 SSNYLLAALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIEIIEVLEFSSIHSTWITV 120

QY 121 PLTIDRYIAVCHPLKHTVSYPARTKRVIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180
DB 121 PLTIDRYIAVCHPLKHTVSYPARTKRVIVSVYITCFLTSIPYVWPNWTEDYISTSVH 180

QY 181 HVLWIHCFTVYLVPSCIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240
DB 181 HVLWIHCFTVYLVPSCIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISFATL 240

QY 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRWLHMSDIANMLALNTAINPFLYCFISKRFRTMAAATL 300

QY 301 KAFFKCKQKQVQFYTNHNSITSSPWISPANSHCIKMLVYQYDKNGKPIK 350
DB 301 KAFFKCKQKQVQFYTNHNSITSSPWISPANSHCIKMLVYQYDKNGKPIK 350

RESULT 14
US-09-995-225-16
; Sequence 16, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human
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; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9e1 Sequence
US-09-995-225-16
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Query Match          94.4%; Score 1857; DB 10; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.4e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLLCLGLPANILTVIILSQLVARROK 60
Db      1 MEHTHAHLAANSSLSWSPGSGACGLGFVPVYVYSLLLCLGLPANILTVIILSQLVARROK 60

QY      61 SSYNVLLALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIIEVLEFSSIHSTIWTIV 120
Db      61 SSYNVLLALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIIEVLEFSSIHSTIWTIV 120

QY      121 PLTIDRYIAVCHPLKXHTVSYPARTRKVIVSVYITCFLTSIPYYWPNWTEDYISTSVH 180
Db      121 PLTIDRYIAVCHPLKXHTVSYPARTRKVIVSVYITCFLTSIPYYWPNWTEDYISTSVH 180

QY      181 HVLWIHCHFTVYLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
Db      181 HVLWIHCHFTVYLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240

QY      241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRPRTMAAATL 300
Db      241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRPRTMAAATL 300

QY      301 KAFFKCKQKQVQFYTNHNFSTSSPWI SPANSHCIKMLVYQYDKNGKPIK 350
Db      301 KAFFKCKQKQVQFYTNHNFSTSSPWI SPANSHCIKMLVYQYDKNGKPIK 350
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RESULT 15

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US-10-094-417-2
; Sequence 2, Application US/10094417
; Publication No. US20030045685A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
```

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; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030045685A1e1 Receptors
; FILE REFERENCE: 018781-008110US
; CURRENT APPLICATION NUMBER: US/10/094,417
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/802,803
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/276,649
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR20
US-10-094-417-2
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Query Match          94.4%; Score 1857; DB 14; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.4e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 SSYNVLLALAAADILVLFVDFVDFLEDFILNMQMPQVPDKIIIEVLEFSSIHSTIWTIV 120
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QY      181 HVLWIHCHFTVYLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
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QY      241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRPRTMAAATL 300
Db      241 WAPRIIMILYHLYGAPIQNRWLHIMSDIANMLALNTAINFFLYCFISKRPRTMAAATL 300

QY      301 KAFFKCKQKQVQFYTNHNFSTSSPWI SPANSHCIKMLVYQYDKNGKPIK 350
Db      301 KAFFKCKQKQVQFYTNHNFSTSSPWI SPANSHCIKMLVYQYDKNGKPIK 350
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Search completed: February 8, 2005, 18:31:28
Job time : 131 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 12, 2005, 13:28:42 ; Search time 588 Seconds
(without alignments)
3732.944 Million cell updates/sec

Title: US-10-689-832-20
Perfect score: 1967
Sequence: 1 MEHTHAHLAANSSLSWSPG.....NDKSSYQFIDAIGACVIL 372

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1967	100.0	1119	10	US-09-813-432-19
2	1967	100.0	1119	17	US-10-174-364-19
3	1967	100.0	1119	17	US-10-246-583-19
4	1967	100.0	1119	18	US-10-689-832-19
5	1967	100.0	1130	17	US-10-333-946-25
6	1967	100.0	1298	16	US-10-314-076-1
7	1939.5	98.6	1110	16	US-10-314-076-3
8	1939.5	98.6	2189	14	US-10-219-834-6
9	1907	96.9	2117	18	US-10-779-104-1
10	1903	96.7	1343	10	US-09-813-432-21
11	1903	96.7	1343	17	US-10-174-364-21
12	1903	96.7	1343	17	US-10-246-583-21
13	1903	96.7	1343	18	US-10-689-832-21
14	1879	95.5	1526	14	US-10-012-140-10
15	1857	94.4	1059	17	US-10-450-590-1
16	1857	94.4	1062	9	US-09-995-225-15
17	1857	94.4	1062	10	US-09-995-225-15
18	1857	94.4	1062	17	US-10-296-294A-3
19	1857	94.4	1062	17	US-10-296-294A-4
20	1857	94.4	1202	14	US-10-094-417-1
21	1829	93.0	1062	14	US-10-012-140-12
22	1741	88.5	1038	14	US-10-094-417-19
23	1732	88.1	1062	17	US-10-450-590-9
24	1673	85.1	1826	17	US-10-450-590-6
25	1628	82.8	957	17	US-10-174-364-84
26	1628	82.8	957	17	US-10-246-583-84
27	1623	82.5	1002	15	US-10-079-384-25
28	1623	82.5	1032	17	US-10-450-590-5
29	1623	82.5	1070	17	US-10-450-590-4
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31	1471	74.8	864	10	US-09-791-932-6
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33	912	46.4	930	10	US-09-791-932-3
34	742	37.7	1466	17	US-10-328-916-4
35	737	37.5	1125	9	US-09-995-225-5
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37	737	37.5	1427	14	US-10-094-417-13
38	737	37.5	1530	13	US-10-011-147-1
39	737	37.5	1793	17	US-10-328-916-3
40	737	37.5	1962	17	US-10-333-946-29
41	733	37.3	1125	14	US-10-012-140-15
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43	668	34.0	34118	15	US-10-017-161-1071
44	668	34.0	34118	17	US-10-292-798-909
45	248	12.6	1650	18	US-10-489-425-49

ALIGNMENTS

RESULT 1
US-09-813-432-19
Sequence 19, Application US/09813432
Publication No. US20030148485A1
GENERAL INFORMATION:
APPLICANT: Taupier Jr., Raymond J
APPLICANT: Majmuder, Kamud
APPLICANT: Spaderna, Steven K
APPLICANT: Smithson, Glenda
APPLICANT: Mezes, Peter S
APPLICANT: Vernet, Corine A. M.
TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
FILE REFERENCE: 15966-729
CURRENT APPLICATION NUMBER: US/09/813,432
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,835
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/190,768
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/190,972


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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1116)
US-10-174-364-19

Alignment Scores:
Pred. No.: 2,94e-191 Length: 1119
Score: 1967.00 Matches: 372
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-689-832-20 (1-372) x US-10-174-364-19 (1-1119)

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DB 1 ATGGAGCACAGCAGCAGCCACCTCGCAGCCAAACAGCTCGCTGTCTTGGTGGTCCCGGC 60

QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrSerLeuLeuLeuCysLeuGly 40
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QY 41 LeuProAlaAsnIleLeuThrValIleLeuSerGlnLeuValAlaAArgGlnLys 60
DB 121 TTACGACGAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAGAGACAGAG 180

QY 61 SerSerTyrAsnTyrLeuLeuAlaAlaAAspIleLeuValLeuPhePheIle 80
DB 181 TCTCTTACAACATATCTCTTGGCAGCTCGCTGCTGCGCAGCATCTTGGTCTCTTTTCA 240

QY 81 ValPheValAspPheLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
DB 241 GTGTTGTGGATCTCTGTGTGAAGATTTCACTTGAAACATGCAGATGCTCAGGTCCC 300

QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
DB 301 GACAGATCATAGAGTGTGGAAATCTCATCTCATCCACCTCCATATGATGATCTGTA 360

QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
DB 361 CGGTTAAACATTGACAGGTATATCGCTGTGCTGCCACCGCTCAAGTACCACAGGTCTCA 420

QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
DB 421 TACCCAGCCCGCACCCGGAAGTCATTGTAAGTGTATTACATCACCTGCTTCTGACCCAGC 480

QY 161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
DB 481 ATCCCTATTACTGGTGGCCCAACATCTGAGCTGAAGACTATCATGACCTCTGTGCTAT 540

QY 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
DB 541 CAGCTCTCATCTGGATCCACTGCTTACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
DB 601 ATCTTGAATCAATCATCTTGTGTACAGCTCAGAGGAGAGCAATTTTGTCTCGGTGCG 660

QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
DB 661 TACTCCAGGGGAGACACCGCCATCTTGTTCACCATTTACCTTCATCTTTCACCATTT 720

QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyValProIleGlnAsnArg 260
DB 721 TGGGCCCCCGCATCATCATGATTTCTTTACCACTCTATGCGGCGCCCATCCAGAACCGC 780

QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
DB 781 TGGCTGGTACATCATGTCCGACATTTGCCAATGCTAGCCCTTCTGAAACAGACCATC 840

QY 281 AsnPheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
DB 841 AACTTCTCTCTACTGCTTTCATCAGCAAGCGTTCCGACCATCGCCAGCCGCGCTC 900

QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
DB 901 AAGGCTTTCTTCAAGTGGCAGAACCTGTACAGTTCTACCAATATAAATTTTTC 960

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RESULT 3
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; Sequence 19, Application US/10246583
; Publication No. US20040058862A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP3CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(1116)
US-10-246-583-19

Alignment Scores:
Pred. No.: 2,94e-191 Length: 1119
Score: 1967.00 Matches: 372
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-689-832-20 (1-372) x US-10-246-583-19 (1-1119)

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Db      1  ATGGAGCACACGACGCGCCACCTCGACCCACCAACAGCTCGTGTCTTGGTGTCCCGCGC 60
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Db      61  TCGGCTGCGGCTTGGGTTTGGTGGCCGCGTGTCTACTACAGCCTCTTGTCTGTGCTCGGT 120
QY      41  LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAspArgGlnLys 60
Db      121  TTACCAAGCAATATCTTGACAGTGAATCTCTCCAGCTGGTGGCAAGACAGAGAAG 180
QY      61  SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
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QY      121  ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
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QY      201  IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
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QY      241  TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyValaProIleGlnAsnArg 260
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QY      261  TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
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QY      341  GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerTyrGln 360
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; Sequence 19, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Majmudar, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729DIV1
; CURRENT APPLICATION NUMBER: US/10/689,832
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
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; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-832-19
Alignment Scores:
Pred. No.: 2.94e-191 Length: 1119
Score: 1967.00 Matches: 372
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
US-10-689-832-20 (1-372) x US-10-689-832-19 (1-1119)
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Db      1  ATGGAGCACACGACGCGCCACCTCGACCCACCAACAGCTCGTGTCTTGGTGTCCCGCGC 60
QY      21  SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db      61  TCGGCTGCGGCTTGGGTTTGGTGGCCGCGTGTCTACTACAGCCTCTTGTCTGTGCTCGGT 120
QY      41  LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAspArgGlnLys 60
Db      121  TTACCAAGCAATATCTTGACAGTGAATCTCTCCAGCTGGTGGCAAGACAGAGAAG 180
QY      61  SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
Db      181  TCCTCTACAACTATCTCTTGGCACTCGTGTGCGGACATCTTGGTCTCTTTTCATA 240
QY      81  ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db      241  GTGTTGTGGACTTCTCTGTGAAGATTTCTATCTTGAACATGCAGATGCCTCAGGTCCC 300
QY      101  AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
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Db 301 GACAGATCATGAGTGTGGAAATTCATCATCCACACCTCCATATGGATTACTGTA 360
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db 361 CCGTTAAACCATTCAGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACACACGGTCTCA 420
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 421 TACCCAGCCGACCCCGGAAGTCAATGTAAGTGTATTACATCACCTGCTTCTCGACACG 480
Qy 161 IleProTyrTyrTrpTrpProLeuIleThrThrGluAspTyrIleSerThrValHis 180
Db 481 ATCCCTATTACTGGTGGCCCAACATCTGACCTGAAGACTTACATAGCACCTCTGTCAT 540
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 541 CAGTCTCATCTGGATCCACTGCTTCCGGTCTACCTTGGTGGCTGCTCCATCTCTTC 600
Qy 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
Db 601 ATCTTGAACCTCAATCATTTGTGTCAAGCTCAGGAGGAAGCAATTTTCTGCTCCGTG 660
Qy 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 661 TACTCACGGGGAAGACACCGCATCTTGTTCACCATTTACCTCCATCTTTGCCACACTT 720
Qy 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
Db 721 TGGGCCCCCGCATCATCATGATCTTTACCACTCTATGGGGGGCCCATCCAGAACCG 780
Qy 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 781 TGGCTGGTACACATCATGCTCCGACATGTCGCAACATGCTAGCCCTTCTGAACACAGCATC 840
Qy 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 841 AACTTCTTCTCTACTGCTTCTATCAGCAAGCGGTTCGACACATGGCAGCCGCAAGCTC 900
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 901 AAGGCTTCTTCAAGTGCAGAGCAAGCACTGTACAGTCTTACACCATCATTAACCTTTCC 960
Qy 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 961 ATAACAAGTAGCCCTCGATCTCGCCGCAAACTCACACTGCATCAAGATGCTGGGTAC 1020
Qy 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerThrGln 360
Db 1021 CAGTATGACAAAATGGAAAACCTATAAAAAGTCGTAATGACAGCAAAAGCTCTTACCAG 1080
Qy 361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
Db 1081 TTTGAAGATGCCATTGGAGCTGTGTCTATCTCTG 1116

RESULT 5

US-10-333-946-25
; Sequence 25, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULET, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946

; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474767CBI
US-10-333-946-25

Alignment Scores:

Pred. No.: 2,996-191 Length: 1130
Score: 1967.00 Matches: 372
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-689-832-20 (1-372) x US-10-333-946-25 (1-1130)

Qy 1 MetGluHisThrHisAlaHisLeuAlaAlaAsnSerLeuSerTrpTrpSerProGly 20
Db 12 ATGGAGCACACGACGCCACCTCCAGCCAAACAGCTGCTGTCTTGGTGGTCCCCGGC 71
Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 72 TCGGCTCGGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 131
Qy 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAlaArgGlnLys 60
Db 132 TTACCAGCAAAATATCTTGACAGTGTATCTCTCTCCAGCTGGTGGCAAGACAGAG 191
Qy 61 SerSerTyrAsnTyrLeuLeuAlaAlaAlaAspIleLeuValLeuPhePheIle 80
Db 192 TCCTCTCAACATATCTCTTGGCACTCGCTGGCGACATCTGGTCTCTCTTTTCA 251
Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 252 GTGTTTGGACTTCTCTGTGGAGATTTCTATCTTGAACATGCAGATGCCTCAGGTCCC 311
Qy 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
Db 312 GACAGATCATAGAGAGTGTGGATTCATCATCCACACCTCCATATGGATTATGTA 371
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysThrHisThrValSer 140
Db 372 CGTTAACCATTTGACAGGTATATCTCTTGGCCACCCGCTCAGTACACACCGGTCTCA 431
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 432 TACCAGCCCGCACCCCGGAAGTCAATGTAAGTGTATTACATCACCTGCTCTCTGACCAG 491
Qy 161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
Db 492 ATCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 551


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QY 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 552 CAGGCTCTCATCTGGATCCATCGCTTACCGGCTACCTGGTGGCCCTGCTCAATCTCTTC 611
QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
Db 612 ATCTTGAACCTCAATCATTTGTGTACAGCTCAGAGAGAGAGCAATTTTCGCTCCGTGGC 671
QY 221 TyrSerThrGlySerThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 672 TACTCCACGGGAGAGACACCCCATCTTGTTCACCAATTTACCTCCATCTTTGCCACACTT 731
QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisIleTyrGlyAlaProIleGlnAsnArg 260
Db 732 TGGGCCCCCGCATCATCATGATTTTACCACTCTATGGGGCGCCCATCCAGAACCGC 791
QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 792 TGGCTGGTACACATCATGTCCGACATTTGCCACATGCTAGCCCTTCTGNAACAGCCATC 851
QY 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 852 AACTTCTTCTCTACTGCTTCAATCAGCAAGCGGTTCCGCACCATGGCAGCGCCACGCTC 911
QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 912 AAGGCTTTCTTCAAGTGGCCAGAACCACTGTACAGTTCTACCAATCAATAACTTTTCC 971
QY 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 972 ATAACAAGTAGCCCTCGATCTCGCGGCAAACTCACATGCATCAAGATGCTGGTGATC 1031
QY 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerSerTyrGln 360
Db 1032 CAGTATGACAAATGGAACCTATAAAAGTCGTAATGACAGCAAAAGCTCTCTACCAG 1091
QY 361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
Db 1092 TTGGAAGATGCCATTTGGAGCTTGTGTATCATCTCTG 1127

RESULT 6
US-10-314-076-1
; Sequence 1, Application US/10314076
; Publication No. US2003015297A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM34, AND VARIANTS A
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338,371
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1047)..(2162)
; OTHER INFORMATION:
US-10-314-076-1
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Alignment Scores:

Pred. No.:	8,36e-191	Length:	2198
Score:	1967.00	Matches:	372
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

Db 2067 CAGTATGACAAAATGGAACCTATAAAAGTCGTAATGACAGCAAAAGCTCCTACCAG 2126
Qy 361 PheGluAspAlaIleGlyAlaCysValIleLeu 372
Db 2127 TTTGAAGATGCCATTGGAGCTGTGTGCATCATCTG 2162
RESULT 7
US-10-314-076-3
; Sequence 3, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY34, AND VARIANTS A
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338,371
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1107)
; OTHER INFORMATION:
US-10-314-076-3
Alignment Scores:
Pred. No.: 1 91e-188 Length: 1110
Score: 1939.50 Matches: 369
Percent Similarity: 99.19% Conservative: 0
Best Local Similarity: 98.19% Mismatches: 0
Query Match: 98.60% Indels: 3
DB: 16 Gaps: 1
US-10-689-832-20 (1-372) x US-10-314-076-3 (1-1110)
Qy 1 MetGluHisThrHisAlaHisLeuAlaAAsnSerLeuSerTrpTrpSerProGly 20
Db 1 ATGGAGCACAGCCAGCCACCTCGCAGCAGCAGCTCGCTGTCTGGTGGTCCCGGC 60
Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyTrpSerLeuLeuLeuGly 40
Db 61 TCGGCTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
Qy 41 LeuProAlaAsnIleLeuThrValIleLeuSerGlnLeuValAlaAargGlnLys 60
Db 121 TTACCAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAGAGACAGAG 180
Qy 61 SerSerTyAsnTyLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePhe 80
Db 181 TCCTCTACAACTATCTCTGGCACTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 240
Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 241 GGTGTGGGATCTCTGTGGAGAAATTCATCTTGAACATGACATGCTCAGGTCCCG 300
Qy 101 AspyIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
Db 301 GACAAGATCATAGAAGTGTGAATTCATCATCATCCACCTCCATATGATGATCTGA 360
Qy 121 ProLeuThrIleAspArgTyIleAlaValCysHisProLeuTyHisThrValSer 140
Db 361 CGGTAAACCATTTGACAGGTATATCGCTGTCTGCCCGCTCAAGTACCACACGCTCA 420
Qy 141 TyTrpAlaArgThrArgLysValIleValSerValIleThrCysPheLeuThrSer 160
Db 421 TACCAGCCCGCCAGCCGGAAGTCAATGTGAAGTGTATACATCACCCTGCTTCTGACCAGC 480

Qy 161 IleProTyTrpTrpTrpProAsnIleTrpThrGluAspTyTrpIleSerThrSerValHis 180
Db 481 ATCCCTATTACTGTGGGCCCAACATCTGGACTGAAGACTATACATCAGCACCTCTGTGCAT 540
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyLeuValProCysSerIlePhePhe 200
Db 541 CACGTCCCTCACTGTGATCCACTGCTTACCGTCTACCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 201 IleLeuAsnSerIleIleValTyTrpLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
Db 601 ATCTTGAACCTCATCTTGTGTACAGCTCAGAGAGAGAGCAATTTCTGCTCCGTGGC 660
Qy 221 TyTrpThrGlyThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 661 TACTCCAGGGGAGACACCGCCATCTTGTTCACATTTACCTCCATCTTTCACACACTT 720
Qy 241 TrpAlaProArgIleIleMetIleLeuTyHisLeuTyGlyAlaProIleGlnAsnArg 260
Db 721 TGGGCCCGCCGATCATCATGATTTTACCACCTCTATGGGGCGCCCATCCAGAACCCG 780
Qy 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 781 TGGCTGGTACACATCATCTCCGACATTCGCAACATGCTAGCCCTCTGACACACGCTC 840
Qy 281 AsnPhePheLeuTyTrpCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
Db 841 AACTTCTTCTTCTACTGCTTTCATCAGCAAGGGTTCGACCATGGCAGCCGCGCTC 900
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyThrAsnHisAsnPheSer 320
Db 901 AAGCTTTCTTCAAGTGCAGAGCACTGTACAGTTCTACCAATCATTAACATTTTCC 960
Qy 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyTr 340
Db 961 ATAACAAGTACGCTGATCTCGCGGCAAACTACACTGATCATGATGCTGGTGTATAC 1020
Qy 341 GlnTyAspLysAsnGlyLysProLysSerArgAsnAspSerLysSerSerTyGln 360
Db 1021 CAGTATGACAAAATGGA-----AAAAGTCGTAATGACAGCAAAAGCTCCTACCAG 1071
Qy 361 PheGluAspAlaIleGlyAlaCysValIleLeuLeu 372
Db 1072 TTTGAAGATGCCATTGGAGCTGTGTGCATCATCTG 1107
RESULT 8
US-10-219-834-6
; Sequence 6, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE TH
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219,834
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313,658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 2189
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-219-834-6

Alignment Scores:
Pred. No.: 5,478-188 Length: 2189
Score: 1939.50 Matches: 369
Percent Similarity: 99.19% Conservative: 0
Best Local Similarity: 99.19% Mismatches: 0
Query Match: 98.60% Indels: 3
DB: 14 Gaps: 1

US-10-689-832-20 (1-372) x US-10-219-834-6 (1-2189)

QY 1 MetGluHisThrHisAlaHisLeuAlaAlaAsnSerSerLeuSerTrpTrpSerProGly 20
DB 1047 ATGGAGCACACGACGCCACCTCGACGCAACACCTCGCTGTCTGGTGTCCCGCGC 1106

QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
DB 1107 TCGGCTCGGGCTTGGGTTTCGTGCCGTGTACTACTACAGCTCTTGTCTGTCCGCTCGGT 1166

QY 41 LeuProAlaAsnLeuThrValIleLeuSerGlnLeuValAlaArgGlnLys 60
DB 1167 TTACGAGCAAAATATCTTGACAGTATCATCTCTCCAGCTGTGGCAAGACAGCAAG 1226

QY 61 SerSerTyrAsnTyrLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
DB 1227 TCCTCTACAACTATCTCTGGCACTCGCTGTGGCACTCTTGTCTCTTTTCATA 1286

QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuLeuAsnMetGlnMetProGlnValPro 100
DB 1287 GTGTTGTGGACTTCTGTGGAGATTTCTATCTTGAACATGCAGATGCCTCAGGTCCCC 1346

QY 101 AspyIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
DB 1347 GACAAGATCATAGAAGTGTGGAATCTCATCTCCATCCACCTCCATATGATGATCTGTA 1406

QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
DB 1407 CGTTAAACATGTACAGGTATATCGCTGTGCCACCCGCTCAAGTACCACACGGTCTCA 1466

QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
DB 1467 TACCAGCCCGCACCCGAAAGTCAATTGTAAGTGTATACATCACCTGTCTCTGACACAGC 1526

QY 161 IleProTyrTyrTrpTrpProAsnIleTrpThrGluAspTyrIleSerThrSerValHis 180
DB 1527 ATCCCTTATTACTGTGTGGCCCAACATCTGAGCTGAAGACTACATCAGCACCTCTGTGAT 1586

QY 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
DB 1587 CAGGTCTCATCTGGATCCACTGTCTCACCGTCTACCTGGTGGCTGTCCATCTTCTTC 1646

QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPhaArgLeuArgGly 220
DB 1647 ATCTTGAATCAATATTGTGTACAAAGCTCAGAGAGAAAGCAATTTTCGTCTCGGTGGC 1706

QY 221 TyrSerThrGlyValThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
DB 1707 TACTCCAGGGGAAGACACCCGCATCTGTTCACCATTACCTCCATCTTGGCCACACTT 1766

QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
DB 1767 TGGGCCCCCGCATCATCATGATTCTTTACCACTCTATGGGGCGCCATCCAGAACCGC 1826

QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
DB 1827 TGGCTGGTACACATCATGTCCGACATTTGCCAATGCTAGCCCTCTCTGAAACACAGCCATC 1886

QY 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaAlaThrLeu 300
DB 1887 AACTTCTTCTCTACTGTCTTCTATCAGACAGCGGTTCGGACCATGGACGCCCGCCACGCTC 1946

QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320

DB 1947 AAGCTTTCTTCAAGTCCGAGAACACCTGTACAGTTCTACACCAATCATATACTTTTC 2006

QY 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
DB 2007 ATAACAAGTAGCCCTCGATCTCGCCGCAAACTCACACTGCATCAAGATGCTGTGTAC 2066

QY 341 GlnTyrAspLysAsnGlyLysProIleLysSerArgAsnAspSerLysSerSerTyrGln 360
DB 2067 CAGTATGACAAATATGA-----AAAAGTCTATGACAGCAAAAGCTCTCTACAG 2117

QY 361 PheGluAspAlaIleGlyAlaCysValIleIleLeu 372
DB 2118 TTGAAGATGCCATTGGAGCTTGTGTATCATCATCCTG 2153

RESULT 9
US-10-779-104-1
; Sequence 1, Application US/10779104
; Publication No. US20040161799A1
; GENERAL INFORMATION:
; APPLICANT: Andrew J. Murphy
; APPLICANT: Susan Croll-Kalish
; TITLE OF INVENTION: KOR3like-Proteins and Methods of Modulating KOR3l-Mediated Activi
; FILE REFERENCE: REG 1000A
; CURRENT APPLICATION NUMBER: US/10779,104
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,447
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/495,577
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2117
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-779-104-1

Alignment Scores:
Pred. No.: 1,11e-184 Length: 2117
Score: 1907.00 Matches: 372
Percent Similarity: 83.22% Conservative: 0
Best Local Similarity: 83.22% Mismatches: 0
Query Match: 96.95% Indels: 75
DB: 18 Gaps: 1

US-10-689-832-20 (1-372) x US-10-779-104-1 (1-2117)

QY 1 MetGluHisThrHisAlaHisLeuAlaAsnSerSerLeuSerTrpTrpSerProGly 20
DB 280 ATGGAGCACACGACGCCACCTCGACGCAACACCTCGCTGTCTTGTGTCTCCCGCGC 339

QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
DB 340 TCGGCTCGGGCTTGGGTTTCGTGCCGTGTCTACTACAGCTCTTGTGTGTCTCGGT 399

QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAlaArgGlnLys 60
DB 400 TTACGAGCAAAATATCTTGACAGTATCATCTCTCCAGCTGTGGGCAAGACAGCAAG 459

QY 61 SerSerTyrAsnTyrLeuLeuAlaAlaAlaAspIleLeuValLeuPhePheIle 80
DB 460 TCCTCTTACAACTATCTTGGCACTCGCTGTCCGACATCTTGGTCTCTTTTCATA 519

QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
DB 520 GTGTTGTGGACTTCTGTGTGAAAGATTTCTATCTTGAACATGCAGATGCCTCAGGTCCCC 579

QY 101 AspyIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
DB 580 GACAAGATCATAGAAGTGTGGAATTTCTATCCATCCACCTCCATATGATGATCTGTA 639

QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140

Db 640 CCGTTAACCAATTGACAGGTATATCGCTGTCGCCACCCGCTCAAGTACACACGGTCTCA 699
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 700 TACCCAGCCCGACCGGAAGTCATTGTAAGTGTATTACATCACTGCTCTCTGACCAGC 759
Qy 161 IleProTyrTyrTrpTrpProIleThrThrGluAspTyrIleSerThrSerValHis 180
Db 760 ATCCCTATTACTGTGTGGCCCAACATCTGGAAGTGAAGACTACATCAGCACCTCTGTGCAT 819
Qy 181 HisValLeuIleTrpIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 820 CAGGCTCATCTGATGCACCTGCTTACCGTCTACCTGGTGGCCCTGCTCCATCTCTTC 879
Qy 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220
Db 880 ATCTTGAAGTCAATCATTTGTGTACAGCTCAGGAGGAGCAATTTTGGTCTCGTGGC 939
Qy 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 940 TACTCCAGGGGAAGACCAACCGCCATCTTGTTCACCAATTACCTCCATCTTTGCCACACTT 999
Qy 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyValProIleGlnAsnArg 260
Db 1000 TGGGCCCCCGCATCATCATGATTTCTTACCACCTCTATGGGGCGCCCATCCAGAACCGC 1059
Qy 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db 1060 TGGCTGTGTGCATCATGTCCGACATTTGCCACATGCTAGCCCTTCTGNACACACCCATC 1119
Qy 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaAlaThrLeu 300
Db 1120 AACTTCTTCTCTACTGCTTCTATCAGCAAGCGTTCCGACCATGGCAGCGCCACGCTC 1179
Qy 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db 1180 AAGGCTTTTCTTCAAGTGGCAGAAAGCAACCTGTACAGATTTCTACCAACATCAATCTTTC 1239
Qy 321 IleThrSerSerProTrpIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db 1240 ATAACAGTAGCCCTTGGATCTCGCGGCAAACTCACACTGCATCAGATGCTGGTGTAC 1299
Qy 341 GlnTyrAspLysAsnGlyLysProIleLys----- 350
Db 1300 CAGTATGACAAATAGGAAACCTATAAAGTATCCCGTGATCCCATAGGTGGCAAC 1359
Qy 350 ----- 350
Db 1360 TACTGCCTCTGTCTAATCCATTTCCAGATGGGAAGGTGTCCATCTATGGCTGAGCAGC 1419
Qy 350 ----- 350
Db 1420 TCTCCTTAAGAGTGCTAATCCGATTTCTGTCTCCGCGAGACTGGGCAATTTCTGAGCTG 1479
Qy 350 ----- 350
Db 1480 GTAGATGAGACAGATGGAAGAGAGAAAGAGAGCATGAAGCTTGTTTTACTTATGCA 1539
Qy 351 -----SerArgAsnAspSerLysSerSerTyrGlnPheGluAspAlaIleG 366
Db 1540 TTTATTTCCACAGAGTCGTAATGACAGCAAAAGCTCTACCAAGTTTGAAGATGCCATTGG 1599
Qy 366 ValaCysValIleIleLeu 372
Db 1600 AGCTGTGTGCATCATCTCTG 1618

RESULT 10

US-09-813-432-21
; Sequence 21, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud

; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-432-21

Alignment Scores:
Pred. No.: 1,41e-184 Length: 1343
Score: 1903.00 Matches: 371
Percent Similarity: 83.00% Conservative: 0
Best Local Similarity: 83.00% Mismatches: 1
Query Match: 96.75% Indels: 75
DB: 10 Gaps: 1

US-10-689-832-20 (1-372) x US-09-813-432-21 (1-1343)

Qy 1 MetGluHisThrHisAlaHisLeuAlaAlaHisSerSerLeuSerTyrTrpSerProGly 20
Db 2 ATGGAGCACACGACGCGCCACCTCGACGCCAACAGCTCGCTGCTTGGTGGTCCCGCGC 61
Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 62 TCGGCTCGCGCTTGGGTTTCTGTCCTTACTACAGCTTCTGTCCTCGGT 121
Qy 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaArgArgGlnLys 60
Db 122 TTACAGCAATATCTTTCAGAGTATCATCTCTCCAGCTGGTGGCAGAGACAGAG 181
Qy 61 SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
Db 182 TCCCTCTACAACTATCTCTTGGCACTCGCTGCGGACATCTTGGTCTCTCTTTTTCATA 241
Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 242 GTGTTTGTGGAGTCTTCTGTTGGAAGATTTCATTTGAACATGCAGATGCCTCAGTCC 301
Qy 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
Db 302 GACAGATCATAGAGTGTCTGGAATCTTCATCCACCTCCATCATATGGAATTTCTGTA 361
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140

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|||||
362 CGGTTAACCATGACAGGTATATCACTGCTGCCACCGCTCAAGTACCACACGGTCTCA 421
QY TyrProAlaAthrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db TACCAGCCCGCACCGGAAAGTCATTGTAAGTGTTTACATCACCTGCTTCTGACCAAGC 481
QY IleProTyrTyrTyrTyrProAsnIleThrPheThrGluAspTyrIleSerThrSerValHis 180
Db ATCCCTATTACTGCTGCGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGGCAT 541
QY HisValLeuIleThrIleHisCysPheThrValTyrIleuValProCysSerIlePhePhe 200
Db CAGCTCCTCATCTGGATCATCTGCTTACCGCTTACCTGGTGGCCGTGCTCCATCTTCTTC 601
QY IleLeuAsnSerIleIleValTyrIysLeuArgLysSerAsnPheArgLeuArgGly 220
Db ATCTTGAACCTCAATCATTTGTGTACAAGCTCAGGAGGAAGACAAATTTTCGTCCGTGGC 661
QY TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrIleu 240
Db TACTCCAGGGGAAGACACCGCCCATCTTGTTCACCATTTACCTCCATCTTTGCCACACTT 721
QY TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
Db TGGGCCCCCGCATCATCATGATCTTTTACCACTTATGGGGGCCCATCCAGNACCGC 781
QY TrpLeuValHisIleMetSerAspIleAlaIleAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
Db TGGCTGGTACACATCATCTCGACATTCGCCAATGCTAGCCCTTCTGAACACAGCCATC 841
QY AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrIleu 300
Db AACTTCTTCTCTACTGCTTATCAGCAAGCGGTTCGCCACATGGCAGCGCCACGCTC 901
QY LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
Db AAGGCTTCTTCAAGTGCAGAGCAACACTGTACAGTTCTACAGTCTACCAACATCAACTTTC 961
QY IleThrSerSerProTyrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
Db ATAAACAAGTAGCCCTGGATCTCGCGCGCAAACTCACACTGCATCAAGATGCTGTGTATC 1021
QY GlnTyrAspLysAsnGlyLysProfile-Lys----- 350
Db CAGTATGACAAATAATGGAAACCTATAAAAGTATATCCCGTGATTCATAGGTGTGGCAAC 1081
QY 350 ----- 350
Db TACTGCCCTCTGTCTAATCCATTTCCAGATGGGAGGTGTCCCATCTATGCTGAGCAGC 1141
QY 350 ----- 350
Db TCTCCTTAAGAGTGTAAATCCGATTTCTGTCTCCCGCAGACTGGGCAATTCCTCAGACTG 1201
QY 350 ----- 350
Db CTAGATGAGAAGAGATGGAAGAGAGAAAGGAGAGCATGAAGCTTTGTTTACTTATGCA 1261
QY 351 -----SerArgAsnAspSerLysSerSerTyrGlnPheGluAspAlaIleG1 366
Db TTTATTTCCACAGAGTGTGTAATGACAGCAAAAGCTCTCATCCAGTTTGAAGATGCCATTGG 1321
QY yAlaCysValIleIleLeu 372
Db AGCTTGTGTCATCATCTG 1340
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RESULT 11

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US-10-174-364-21
; Sequence 21, Application US/10174364
; Publication No. US20030216308A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
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; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-725CIP2
; CURRENT APPLICATION NUMBER: US/10/174,364
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 21
; LENGTH: 1343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1060)
US-10-174-364-21
Alignment Scores:
Pred. No.: 1,41e-184 Length: 1343
Score: 1903.00 Matches: 371
Percent Similarity: 83.00% Conservative: 0
Best Local Similarity: 83.00% Mismatches: 1
Query Match: 96.75% Indels: 75
DB: 17 Gaps: 1
US-10-689-832-20 (1-372) x US-10-174-364-21 (1-1343)
QY 1 MetGluHisThrHisAlaHisLeuAlaAsnSerSerLeuSerTyrTrpSerProGly 20
Db 2 ATGGAGCACAGCAGCGCCACCTCGCAGCCAAACAGCTCGCTGTCTTGGTGGTCCCCGGC 61
QY 21 SerAlaCysGlyLeuGlyPheValProValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 62 TCGGCCTCGCGCTTGGGTTTGGTCCCGTGGTCTTACTACAGCCCTTTGCTGTGCTCGGT 121
QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaArgArgGlnLys 60
Db 122 TTACAGCAATAATCTTGACAGTGATCATCTCTCCAGCTGGTGGCAGACAGAG 181
QY 61 SerSerTyrAenTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
Db 182 TCCTCTTACACTATCTCTTGGCACTCGTCTGCCGACATCTTGGTCTCTTTTTCATA 241
QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
Db 242 GTGTTTGGGACTTCTCTTGGAAAGATTTCATCTTGAACATGCGAGATGCCCTCAGGTCCCC 301
QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTrpIleThrVal 120
Db 302 GACAGATCATAGAGTGCTGGAATTTCTCATCCATCCACACTCCATATGATGATCTGTA 361
QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db 362 CCGTTAACCATTTGACAGGTATATCACTGCTTGGCCCGGCTCAAGTACCACACGGTCTCA 421
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QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
| | | | |
Db 422 TACCACGCGCGCACCGGAAAGTCAATTGTAAGTGTATACATCACTGCTCTCTGACGAGC 481
| | | | |
QY 161 IleProTyrTyrTrpTrpProAlaIleThrThrGluAspTyrIleSerThrSerValHis 180
| | | | |
Db 482 ATCCCTATTACTGCGGGGCCCAACATCTGAGCTGAAGACTTACATCAGCAGCCTCTGTGCAT 541
| | | | |
QY 181 HisValLeuIleThrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
| | | | |
Db 542 CAGTCTCTATCTGGATCACTGCTTACCGTCTACTGTGTCCTGCTCCATCTCTCTTC 601
| | | | |
QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgArgLysSerAsnPheArgLeuArgGly 220
| | | | |
Db 602 ATCTGAACCTCAATCATTTGTGTACAAGCTCAGGAGGAGCAATTTTCGTCTCCGTGCG 661
| | | | |
QY 221 TyrSerThrGlyThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
| | | | |
Db 662 TACTCACGGGGAGAACCAACCGCCATCTTGTTCACCAATTACCTCCATCTTTGCCACAT 721
| | | | |
QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
| | | | |
Db 722 TGGGCCCCCGCATCATGATGATCTTTTACCCTCTATGGGGCGCCATCCAGAACCCG 781
| | | | |
QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
| | | | |
Db 782 TGGCTGGTACACATCATGTCGACATTTGCCAATGCTAGCCCTTCTGAACACAGCCATC 841
| | | | |
QY 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaIleThrLeu 300
| | | | |
Db 842 AACTTCTCTCTACTGCTTCTATCATCAGCAAGCGGTTCGCCACCATGTCAGCGCCAGCTC 901
| | | | |
QY 301 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
| | | | |
Db 902 AAGGCTTCTTCAAGTGCAGAGCAAGCACTGTACAGTTCTACACCAATCATTAACCTTTCC 961
| | | | |
QY 321 IleThrSerSerProThrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
| | | | |
Db 962 ATAACAAGTAGCCCTTGGATCTCGCGCGCAAACTCACACTGCATCAAGATGCTGTGTATC 1021
| | | | |
QY 341 GlnTyrAspLysAsnGlyLysProIle-Lys----- 350
| | | | |
Db 1022 CAGTATGACAAAATGGAAGAACCTATAAAGTATCCCGTGATTCCTATAGGTGTGCGAAC 1081
| | | | |
QY 350 ----- 350
| | | | |
Db 1082 TACTGCCTCTGTAACTCAATTCAGATGGGAAGGTGCCATCTATGGCTGAGCAGC 1141
| | | | |
QY 350 ----- 350
| | | | |
Db 1142 TCTCCTTAAGAGTGTAAATCCGATTTCCTGTCCTCCGAGAGCTGGGCAATCTCAGACTG 1201
| | | | |
QY 350 ----- 350
| | | | |
Db 1202 GTAGATGAGAGAGATGGGAAGAGAGAAAGGAGAGCATGAAGCTGTTTTTACTTATGCA 1261
| | | | |
QY 351 -----SerAtqAsnAspSerLysSerTyrGlnPheGluAspAlaIleG 366
| | | | |
Db 1262 TTTATTTCCAGAGTCTGTAATGACAGCAAAAGCTCTTACCAGTTTGAAGATGCCATTGG 1321
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QY 366 yAlaCysValIleIleLeu 372
| | | | |
Db 1322 AGCTTGTGTATCATCTCTG 1340
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RESULT 12

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US-10-246-583-21
; Sequence 21, Application US/10246583
; Publication No. US20040058862A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
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; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1060)
US-10-246-583-21
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Alignment Scores:

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Pred. No.: 1.41e-184 Length: 1343
Score: 1903.00 Matches: 371
Percent Similarity: 83.00% Conservative: 0
Best Local Similarity: 83.00% Mismatches: 1
Query Match: 96.75% Indels: 75
DB: 17 Gaps: 1
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US-10-689-832-20 (1-372) x US-10-246-583-21 (1-1343)

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QY 1 MetGluHisThrHisAlaHisLeuAlaAlaAsnSerSerLeuSerTyrTrpSerProGly 20
| | | | |
Db 2 ATGGAGCAACAGCAGCCACCCTCCAGCCAAACAGCTCGCTGCTGTGGTGGTCCCCCGGC 61
| | | | |
QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuGly 40
| | | | |
Db 62 TCGGCTCGGCTTGGGTTTCGTGCGCGTGGTCTACTACAGCTCTTGTGTGCTCGGT 121
| | | | |
QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaArgArgGlnLys 60
| | | | |
Db 122 TTACAGCAAAATATCTTGACAGTGATCATCTCTCCAGCTGTGGTGGCAAGACAGAG 181
| | | | |
QY 61 SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
| | | | |
Db 182 TCTCTCTACAACTATCTCTTGGCACTCGCTGCTGCCAGACATCTTGTCTCTTTTCATA 241
| | | | |
QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
| | | | |
Db 242 GTGTTTGGGACTTCTCTGTGGAGATTTCATCTTGAACATGCAGATGCCTCAGGTCCCC 301
| | | | |
QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleThrIleThrVal 120
| | | | |
Db 302 GACAAGATCATAGAAGTGTGGAAATTCATCTCCATCCACCTCCATATGGATTATGTA 361
| | | | |
QY 121 ProLeuThrIleAspAtqTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
| | | | |
Db 362 CCGTTAACCATGTACAGGTATATCACTGTCTGCCACCCGCTCAAGTACCACAGGTCTCA 421
| | | | |
QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
| | | | |
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422	Db	 TACCACGCGGCACCGGAAAGTCATTGTAAGTGTTTACATCACTGCTTCTGTCCAGCCAGC	481
161	Qy	 IleProTyrTyrTrpTrpProAsnIleThrThrCluAspTyrIleSerThrSerValHis	180
482	Db	 ATCCCCCTATTACTGTGTGGCCCAACATCTGACACTGAAGACTACATCAGCACTCTGTGCAT	541
181	Qy	 HisValLeuIleTrrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe	200
542	Db	 CACGTCTCATCTGGATCCACTGCTTACCGTCTACCTGTGCGCTGCTCCATCTTCTTC	601
201	Qy	 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly	220
602	Db	 ATCTTGAATCAATCATTTGTGTAACAGCTCAGGAGGAAGCAATTTTGTCTCCGTGGC	661
221	Qy	 TyrSerThrGlyLysThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu	240
662	Db	 TACTCCACGGGGAAGACACCGCCATCTTGTTCACCATTAACCTCCATCTTTGGCACACTT	721
241	Qy	 TrrAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg	260
722	Db	 TGGGCCCCCGGCATCATCATGATTCTTTTACCCCTCTATGGGCGGCCATCCAGAACCCG	781
261	Qy	 TrrLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle	280
782	Db	 TGGCTGTGTACATCATGTCCGACATGGCCACATGTCTAGCCCTTCTGAAACAGCCATC	841
281	Qy	 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu	300
842	Db	 AACTTCTTCTCTACTGCTTCATCAGCAAGCGGTTCGCACCATGGCAGCGCCACGCCTC	901
301	Qy	 LysAlaPhePheLysCysGlnLysGlnProValGlnPheTyrThrAsnHisAsnPheSer	320
902	Db	 AAGGCTTCTTCAAGTGCCGAAGCAACCTGTACAGTTCTACACCAATCATATACTTTTCC	961
321	Qy	 IleThrSerSerProTrrIleSerProAlaAsnSerHisCysIleLysMetLeuValTyr	340
962	Db	 ATAACAAGTAGCCCTGGATCTCGCCGGCAAACTCACACTGCATCAAGATGCTGGTGTAC	1021
341	Qy	 GlnTyrAspLysAsnGlyLysProIle-Lys-----	350
1022	Db	 CAGTATGACAAAATGAAAACCTATAAAGATATCCCGTGATTCATAGGTGGCAAC	1081
350	Qy	----- TACTGCTCTGTCTTAATCCATTTCCAGATGGGAAGGTGTCCATCTTATGGCTGAGCAGC	350
1082	Db	----- TCTCCTTAAAGATGCTAATCCGATTTCTCTCTCCGACAGCTGGGCAATTCACAGACTG	1141
350	Qy	----- -----	350
1142	Db	----- TCTCCTTAAAGATGCTAATCCGATTTCTCTCTCCGACAGCTGGGCAATTCACAGACTG	1201
350	Qy	----- -----	350
1202	Db	----- GTAGATGAGAAGAGATGGAAGAGAGAAAGAGAGCATGAAGCTGTGTTTTTACTATGCA	1261
351	Qy	----- -----SerArgAsnAspSerLysSerSerTyrGlnPheGluAspAlaIleG1	366
1262	Db	 TTTTATTCCACAGAGTCGTAAATGACAGCAAAAGCTCTACAGTTTGGAAGATGCCATTG	1321
366	Qy	 yAlaCysValIleIleLeu 372	
1322	Db	 AGCTTGTGTATCATCTCTG 1340	

RESULT 13

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US-10-689-832-21
; Sequence 21, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Majmuder, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729DIV1
; CURRENT APPLICATION NUMBER: US/10/689,832
; CURRENT FILING DATE: 2003-10-20

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Db 482 ATCCCTATTACTGGTGGCCCAACATCTGCACTGAAGACTACATCAGCACCTCTGTGCAT 541
Qy HisValLeuIleThrPheHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 542 CAGTCTCTCATCTGGATCCACTGCTTACCGGTCTACTGTGCTGCTGCTTCTCTTCTTC 601
Qy IleLeuAanSerIleIleValTyrIleValTyrIleValTyrIleValTyrIleValTyr 220
Db 602 ATCTTGAATCAATCATCTGTACAGCTCAGGAGGAGAGCAATTTTGTCTCCGTGCG 661
Qy TyrSerThrGlyValThrAlaIleLeuPheThrIleThrSerIlePheAlaThrIleu 240
Db 662 TACTCCACGGGAGAGACCCCGCATCTTGTTCACCATTTACTCTCCATCTTTGCCACAT 721
Qy TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAanArg 260
Db 722 TGGGCCCCCGCATCATCATGATCTTTTACCATCTATGCGGGCGCCATTCAGAACCGC 781
Qy TrpLeuValHisIleMetSerAspIleAlaAanMetLeuAlaLeuLeuAanThrAlaIle 280
Db 782 TGGCTGGTACACATCATGTCGACATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 841
Qy AanPhePheLeuTyrCysPheIleSerIleValTyrPheArgThrMetAlaAlaThrIleu 300
Db 842 AACTTCTTCTCTACTGCTTCTATCAGCAAGCGGTTCCGACCATTCGACCGCCGACGTC 901
Qy LysAlaPhePheLysCysGlnValProValGlnPheTyrThrAanHisAanPheSer 320
Db 902 AGGCTTTCTTCAAGTCCAGAGCAACCTGTACAGTTCTACCCATCATCACTTTTCTCC 961
Qy IleThrSerSerProThrIleSerProAlaAanSerHisCysIleIleValTyrValTyr 340
Db 962 ATAACAAGTAGCCCTGGATCTCGCGCGCAAACTCACACTGATCAAGATGCTGGTGATC 1021
Qy GlnTyrAspLysAanGlyLysProIleLys----- 350
Db 1022 CAGTATGACAAAATGGAAAACCTATAAAAGTATCCCGGTGATCCATAGTGTGGCAAC 1081
Qy 350 ----- 350
Db 1082 TACTGCCTCTGCTAATCAATTCAGATGGGAAGGTGCCCATCTATGGCTGAGCAGC 1141
Qy 350 ----- 350
Db 1142 TCTCTTAAAGATGCTAATCCGATTTCTGTCTCCGAGACTGGGCAATTCAGACATG 1201
Qy 350 ----- 350
Db 1202 GTAGATGAGAGAGATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261
Qy 351 -----SerArgAanAspSerLysSerTyrGlnPheGluAspAlaIleGln 366
Db 1262 TTTATTTCCAGAGATCGTGAATGACAGAAAAGCTCTTACCAGTTTGAAGATGCCATTGG 1321
Qy 366 yAlaCysValIleIleLeu 372
Db 1322 AGCTGTGTGCATCATCTG 1340
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RESULT 14

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US-10-012-140-10
; Sequence 10, Application US/10012140
; Publication No. US2003009017A1
; GENERAL INFORMATION:
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
; TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 381552004900
; CURRENT APPLICATION NUMBER: US/10/012,140
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 60/246,772
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; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,772
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,185
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (139)...(1200)
US-10-012-140-10

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Pred. No.: 4,97e-182 Length: 1526
Score: 1879.00 Matches: 366
Percent Similarity: 82.33% Conservative: 2
Best Local Similarity: 81.88% Mismatches: 4
Query Match: 95.53% Indels: 75
DB: 14 Gaps: 1

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Qy 1 MetGluHisThrHisAlaHisLeuAlaAanSerSerLeuSerTyrTrpSerProGly 20
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Qy 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
Db 199 TCGGCTCGCGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 258
Qy 41 LeuProAlaAanIleLeuThrValIleIleLeuSerGlnLeuValAlaAanArgGlnLys 60
Db 259 TTACAGCAAAATATCTTGACAGTGTATCTCTCCAGTGTGGTGGTGGTGGTGGTGGTGG 318
Qy 61 SerSerTyrAanTyrLeuLeuAlaAlaAanPheIleLeuValLeuPhePheIle 80
Db 319 TCCTCTCAAACTATCTTGGCACTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 378
Qy 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAanMetGlnMetProGlnValPro 100
Db 379 GTGTTTGGAGCTTCTCTGTGGAGATTTCTATTTGAACATGCAGATGCCTCAGGTCCCC 438
Qy 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleThrIleThrVal 120
Db 439 GACAGATCATAGAGTGTGGATTTCTATCCATCCACCTCCATATATGGATTACTGTGA 498
Qy 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
Db 499 CGGTAAACATTCAGAGGTATATCGTGTGGCACCCTGCTCAAGTACCAGTCCATCTCTTC 558
Qy 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
Db 559 TACCAGCCCGCACCCGGAAGTCTTGAAGTGTATACATCACCTGCTCTCTGACCAGC 618
Qy 161 IleProTyrTyrTrpTrpProAanIleThrGluAspTyrIleSerThrSerValHis 180
Db 619 ATCCCTATTACTGGTGGCCCAACATCTCGAGCTGAAGACTACATCAGCACCTCTGTGCAT 678
Qy 181 HisValLeuIleThrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
Db 679 CACGTCCTCATCTGGGTCCACTGCTTACCCTGCTTACCAGGTGCCCTGCTCTCATCTCTTC 738
Qy 201 IleLeuAanSerIleIleValTyrIleValTyrIleValTyrIleValTyrIleValTyr 220
Db 739 ATCTTGAATCAATCGTGTGTGTACAGCTCAGGAGGAGAGCAATTTTGTCTCTGTGGC 798
Qy 221 TyrSerThrGlyLysThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
Db 799 TACTCCACGGGAGAGACCCCGCATCTTGTTCACCATTTACTCTCCATCTTTGCCATCTT 858
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QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
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QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
DB 919 TGGCTGGTACACATCATGTCCGACATTCGCCAACATGCTAGCCCTCTCTGAAACACAGCCATC 978
QY 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaThrLeu 300
DB 979 AACTTCTTCTCTACTGCTTCTCATCAGCAAGGGTTCCGACCATGGCAGCGCCACGCTC 1038
QY 301 LysAlaPhePheLysCysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
DB 1039 AAGGCTTTCTTCAAGTGCAGAGCACTGTACAGTTCTACCACTCAACATCAATCTTTCC 1098
QY 321 IleThrSerSerProTyrPheSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
DB 1099 ATAACAAGTAGCCCTGGATCTGCGCGGCAAACTCACACTGCATCAAGATGCTGGTGATC 1158
QY 341 GlnTyrAspLysAsnGlyAspProIle-Lys----- 350
DB 1159 CAGTATGACAAAATGGAAAACTATAAAAGTATCCCGGTATTCCATAGGTGGCAAC 1218
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QY 351 -----SerArgAsnAspSerLysSerTyrGlnPheGluAspAlaIleG1 366
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QY 366 yAlaCysValIleIleLeu 372
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US-10-450-590-1
; Sequence 1, Application US/10450590
; Publication No. US20040076985A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN CHEMOKINE-LIKE RECEPTOR
; FILE REFERENCE: LI0316 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/450,590
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/254,923
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US 60/280,110
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/299,474
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-590-1
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Score: 1857.00 Matches: 350
Percent Similarity: 100.00% Conservative: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.41% Indels: 0
DB: 17 Gaps: 0
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DB 1 ATGGAGCACACGACGACCCACCTCGCAGCCACACAGCTCGCTGTCTTGGTGGTCCCCCGGC 60
QY 21 SerAlaCysGlyLeuGlyPheValProValValTyrTyrSerLeuLeuLeuCysLeuGly 40
DB 61 TCGGCTTCGGCTTGGGTTTCGTGCGGTGGTCTACTACAGCCTCTTGTGTGGCTCGGT 120
QY 41 LeuProAlaAsnIleLeuThrValIleIleLeuSerGlnLeuValAlaAArgArgGlnLys 60
DB 121 TTACAGCAATATCTTGGACAGTATCATCTCTCCAGCTGGTGGCAAGAACAGAG 180
QY 61 SerSerTyrAsnTyrLeuLeuAlaLeuAlaAlaAspIleLeuValLeuPhePheIle 80
DB 181 TCCTCTTACAACTATCTCTGGCACTCGCTGCTGCCGACATCTTGGTCTCTTTTCATA 240
QY 81 ValPheValAspPheLeuLeuGluAspPheIleLeuAsnMetGlnMetProGlnValPro 100
DB 241 GTGTTTGTGGACTTCTCTGTTGGAAGATTTCATCTTGAACATGCAGATGCCTCAGGTCCCC 300
QY 101 AspLysIleIleGluValLeuGluPheSerSerIleHisThrSerIleTyrIleThrVal 120
DB 301 GACAAGATCATAGAAAGTGTGGAATCTTCATCCATCCACCTCCATATGATGATCTGTGA 360
QY 121 ProLeuThrIleAspArgTyrIleAlaValCysHisProLeuLysTyrHisThrValSer 140
DB 361 CCGTTAACCATTTGACAGGTATATCGCTGCTGCGCACCGCTCAAGTAGTACCACACGGTCTCA 420
QY 141 TyrProAlaArgThrArgLysValIleValSerValTyrIleThrCysPheLeuThrSer 160
DB 421 TACCAGCCCGCACCCGGAAGTCAATTGTAAGTGTTTACATCACCTGCTCTCTCACCACGC 480
QY 161 IleProTyrTyrTyrTrpProAsnIleTyrThrGluAspTyrIleSerThrSerValHis 180
DB 481 ATCCCTTATTACTGGTGGCCCAACATCTGGACTGAAAGACTACATCAGCACCTCTGTGGAT 540
QY 181 HisValLeuIleTyrIleHisCysPheThrValTyrLeuValProCysSerIlePhePhe 200
DB 541 CACGTCTCTATCTGGATCCACTGCTTCACCGCTTACCTGGGCGCTGCTGCTCATCTCTTCTC 600
QY 201 IleLeuAsnSerIleIleValTyrLysLeuArgLysSerAsnPheArgLeuArgGly 220
DB 601 ATCTTGAACCTCAATCATTTGTGTACAGCTCAGGAGGAGCAATTTTCGTCTCGGTGGC 660
QY 221 TyrSerThrGlyLysThrThrAlaIleLeuPheThrIleThrSerIlePheAlaThrLeu 240
DB 661 TACTCCAGGGGAAGACACCGCCATCTTGTTCACCATTACCTCCATCTTTGGCCACACTT 720
QY 241 TrpAlaProArgIleIleMetIleLeuTyrHisLeuTyrGlyAlaProIleGlnAsnArg 260
DB 721 TGGGCCCCCGCATCATCATGATCTTTTACCACCTCTATGGGGCGCCCATCCAGAACCGC 780
QY 261 TrpLeuValHisIleMetSerAspIleAlaAsnMetLeuAlaLeuLeuAsnThrAlaIle 280
DB 781 TGGCTGGTACACATCATGTCCGACATTTGCCAACATGTAGCCCTTCTGAAACACAGCCATC 840
QY 281 AsnPhePheLeuTyrCysPheIleSerLysArgPheArgThrMetAlaAlaAlaThrLeu 300
DB 841 AACTTCTTCTCTACTGCTTCTCATCAGCAGGGTTCCGACCATGGCAGCGCCACGCTC 900
QY 301 LysAlaPhePheLysCysGlnProValGlnPheTyrThrAsnHisAsnPheSer 320
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QY 321 IleThrSerSerProTyrPheSerProAlaAsnSerHisCysIleLysMetLeuValTyr 340
DB 961 ATAAAGATGAGCCCTGGATCTCGCGGCAAACTCACACTGCATCAAGATGCTGGTGATC 1020
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Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1119	100.0	1119	10	US-09-813-432-19
2	1119	100.0	1119	17	US-10-174-364-19
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4	1119	100.0	1119	18	US-10-689-832-19
5	1119	100.0	1130	17	US-10-333-946-25
6	1119	100.0	2198	16	US-10-314-076-1
7	1091	97.5	1110	16	US-10-314-076-3
8	1091	97.5	2189	14	US-10-219-834-6
9	1050	93.8	1059	17	US-10-450-590-1
10	1050	93.8	1052	17	US-10-296-294A-3
11	1050	93.8	1202	14	US-10-094-417-1
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					Sequence 19, Appl
					Sequence 19, Appl
					Sequence 25, Appl
					Sequence 1, Appl
					Sequence 3, Appl
					Sequence 6, Appl
					Sequence 1, Appl
					Sequence 3, Appl
					Sequence 1071, Ap
					Sequence 909, App
					Sequence 62, Appl

12	1048.4	93.7	1062	9	US-09-995-225-15	Sequence 15, Appl
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14	1048.4	93.7	1062	17	US-10-296-294A-4	Sequence 4, Appl
15	1048.4	93.7	1343	10	US-09-813-432-21	Sequence 21, Appl
16	1048.4	93.7	1343	17	US-10-174-364-21	Sequence 21, Appl
17	1048.4	93.7	1343	17	US-10-246-583-21	Sequence 21, Appl
18	1048.4	93.7	1343	18	US-10-689-832-21	Sequence 21, Appl
19	1048.4	93.7	2117	18	US-10-779-104-1	Sequence 1, Appl
20	1040.4	93.0	1062	14	US-10-012-140-12	Sequence 12, Appl
21	1040.4	93.0	1526	14	US-10-012-140-10	Sequence 10, Appl
22	934.8	83.5	1062	17	US-10-450-590-9	Sequence 9, Appl
23	929.8	83.1	957	17	US-10-174-364-84	Sequence 84, Appl
24	929.8	83.1	957	17	US-10-246-583-84	Sequence 84, Appl
25	926	82.8	1002	15	US-10-079-384-25	Sequence 25, Appl
26	926	82.8	1158	17	US-10-343-650A-21	Sequence 21, Appl
27	922.4	82.4	1032	17	US-10-450-590-5	Sequence 5, Appl
28	922.4	82.4	1070	17	US-10-450-590-4	Sequence 4, Appl
29	922.4	82.4	1826	17	US-10-450-590-6	Sequence 6, Appl
30	844.2	75.4	864	10	US-09-791-932-6	Sequence 6, Appl
31	832	74.4	1038	14	US-10-094-417-19	Sequence 19, Appl
32	756.4	67.6	795	15	US-10-225-567A-586	Sequence 586, App
33	524	46.8	930	10	US-09-791-932-3	Sequence 3, Appl
34	268.2	24.0	1466	17	US-10-328-916-4	Sequence 4, Appl
35	268.2	24.0	1962	17	US-10-333-946-29	Sequence 29, Appl
36	266.6	23.8	1125	9	US-09-995-225-5	Sequence 5, Appl
37	266.6	23.8	1125	10	US-09-995-225-5	Sequence 5, Appl
38	266.6	23.8	1125	14	US-10-012-140-15	Sequence 15, Appl
39	266.6	23.8	1427	14	US-10-094-417-13	Sequence 13, Appl
40	266.6	23.8	1530	13	US-10-011-147-1	Sequence 1, Appl
41	266.6	23.8	1719	14	US-10-012-140-13	Sequence 13, Appl
42	266.6	23.8	1793	17	US-10-328-916-3	Sequence 3, Appl
43	243.8	21.8	34118	15	US-10-017-161-1071	Sequence 1071, Ap
44	243.8	21.8	34118	17	US-10-292-798-909	Sequence 909, App
45	80	7.1	80	14	US-10-219-834-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-813-432-19
; Sequence 19, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1 Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836

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/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 60/193,843
/ PRIOR FILING DATE: 2000-03-31
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 1119
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-813-432-19

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TCGGCTCGGGCTTGGGTTTCGTCGCCGNGTCTACTACAGCCTCTTGTGTGCTCGGT 120

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Db 1021 CAGTATGACAAAATGGAACCTTATAAAAGTCTGTAATGACAGCAAAAGCTCTTACCAG 1080
QY 1081 TTTGAAGATGCCATTTGGAGCTTGTGTATCATCTCTGTGA 1119
Db 1081 TTTGAAGATGCCATTTGGAGCTTGTGTATCATCTCTGTGA 1119
```

RESULT 2

```
US-10-174-364-19
/ Sequence 19, Application US/10174364
/ Publication No. US20030216308A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson et al.
/ TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 15966-729CIP2
/ CURRENT APPLICATION NUMBER: US/10/174,364
/ CURRENT FILING DATE: 2002-06-17
/ PRIOR APPLICATION NUMBER: 60/190,835
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: 60/190,768
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: 60/190,972
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 60/191,199
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 60/191,947
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/192,665
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,657
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,984
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,664
/ PRIOR FILING DATE: 2000-03-28
/ PRIOR APPLICATION NUMBER: 60/192,836
/ PRIOR FILING DATE: 2000-03-29
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 128
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 1119
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1116)
US-10-174-364-19
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Query Match      100.0%; Score 1119; DB 17; Length 1119;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCACAGCAGCCACCTCGAGGCCAACAGCTCGTCTCTTGGTGTCCTCCCGGC 60
Db 1 ATGGAGCACAGCAGCCACCTCGAGGCCAACAGCTCGTCTCTTGGTGTCCTCCCGGC 60

QY 61 TCGGCTCGGGCTTGGGTTTCGTCGCCGNGTCTACTACAGCCTCTTGTGTGCTCGGT 120
Db 61 TCGGCTCGGGCTTGGGTTTCGTCGCCGNGTCTACTACAGCCTCTTGTGTGCTCGGT 120
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Db 841 AACTCTTCTCTTACTGCTTCATCAGCAAGCGGTTCCGACACATGGCAGCCGCGCACGCTC 900
Qy 901 AAGGCTTTCTTCAAGTGCCAGAGCAACCTGTACAGTTCTTACACCAATCATAACTTTTCC 960
Db 901 AAGGCTTTCTTCAAGTGCCAGAGCAACCTGTACAGTTCTTACACCAATCATAACTTTTCC 960
Qy 961 ATAAAGTAGCCCTTGGATCTCGCCGCAAACTCACTGATCAAGATGCTGGGTAC 1020
Db 961 ATAAAGTAGCCCTTGGATCTCGCCGCAAACTCACTGATCAAGATGCTGGGTAC 1020
Qy 1021 CAGTATGACAAAATGAAAACCTATAAAAAGTCGTAATGACAGCAAAAAGCTCCACCAG 1080
Db 1021 CAGTATGACAAAATGAAAACCTATAAAAAGTCGTAATGACAGCAAAAAGCTCCACCAG 1080
Qy 1081 TTGAGAGTGCCTTGGAGCTTGTGTATCATCTCTGTGA 1119
Db 1081 TTGAGAGTGCCTTGGAGCTTGTGTATCATCTCTGTGA 1119

RESULT 5

US-10-333-946-25
; Sequence 25, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474767CB1
US-10-333-946-25

Query Match 100.0%; Score 1119; DB 17; Length 1130;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGCACAGCAGCCCACTCGCAGCAACAGCTCGCTGTCTTGGGTGTCCTCCCGGC 60
|||||

Db 12 ATGGAGCACAGCAGCCCACTCGCAGCAACAGCTCGCTGTCTTGGGTGTCCTCCCGGC 71
Qy 61 TCGGCTCGCGCTTGGGTTTCGTGCCCGTGTACTACTACAGCCTCTTGTGTGCTCGGT 120
Db 72 TCGGCTCGCGCTTGGGTTTCGTGCCCGTGTACTACTACAGCCTCTTGTGTGCTCGGT 131
Qy 121 TTACAGCAAAATATCTTGACAGTGAATCATCTCTCCAGCTGGTGGCAAGACAGAAG 180
Db 132 TTACAGCAAAATATCTTGACAGTGAATCATCTCTCCAGCTGGTGGCAAGACAGAAG 191
Qy 181 TCCTCTCAACAATATCTCTTGGCACTCGCTGTGCGGACATCTTGGTCTCTTTTTCATA 240
Db 192 TCCTCTCAACAATATCTCTTGGCACTCGCTGTGCGGACATCTTGGTCTCTTTTTCATA 251
Qy 241 GTGTTGTGGAGCTTCTGTGTGAAGATTTCACTTTGAACATGACAGATGCTCAGGTCCC 300
Db 252 GTGTTGTGGAGCTTCTGTGTGAAGATTTCACTTTGAACATGACAGATGCTCAGGTCCC 311
Qy 301 GACAAGATCATAGAAGTGTGGAATTTCTCATCTCATCCACCTCCATATGGATTACTGTA 360
Db 312 GACAAGATCATAGAAGTGTGGAATTTCTCATCTCATCCACCTCCATATGGATTACTGTA 371
Qy 361 CGGTTAAACCATTGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACCACACGGTCTCA 420
Db 372 CGGTTAAACCATTGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACCACACGGTCTCA 431
Qy 421 TACCAGCCCGCACCCGGAAGTCAATGTAAAGTGTATATACATCACCTGTCTCTGACACAG 480
Db 432 TACCAGCCCGCACCCGGAAGTCAATGTAAAGTGTATATACATCACCTGTCTCTGACACAG 491
Qy 481 ATCCCTTATCTGTGTGGCCCAACATCTGGAGTGAAGACTATACAGCACTCTGTGCAAT 540
Db 492 ATCCCTTATCTGTGTGGCCCAACATCTGGAGTGAAGACTATACAGCACTCTGTGCAAT 551
Qy 541 CAGGCTCTCATCTGATTCACCTGCTTCAACGCTTACCTGTGCTGCTCCATCTTCTTTC 600
Db 552 CAGGCTCTCATCTGATTCACCTGCTTCAACGCTTACCTGTGCTGCTCCATCTTCTTTC 611
Qy 601 ATCTTGAACCTCAATCATTTGTGTACAGCTCAGAGGAAGAGCAATTTTCTGCTCCGTGGC 660
Db 612 ATCTTGAACCTCAATCATTTGTGTACAGCTCAGAGGAAGAGCAATTTTCTGCTCCGTGGC 671
Qy 661 TACTCCAGGGGAAGACACACCGCCATCTTGTTCACATTTACCTCATCTTTGCGCACATTT 720
Db 672 TACTCCAGGGGAAGACACACCGCCATCTTGTTCACATTTACCTCATCTTTGCGCACATTT 731
Qy 721 TGGGCCCCCGCATCATCATGATTTCTTACCACTCTATGGGGCGCCCATCCAGAACCCG 780
Db 732 TGGGCCCCCGCATCATCATGATTTCTTACCACTCTATGGGGCGCCCATCCAGAACCCG 791
Qy 781 TGGCTGGTACACATCATGTCCGACATTTGCCAATGCTAGCCCTTTCTGAACACAGCCATC 840
Db 792 TGGCTGGTACACATCATGTCCGACATTTGCCAATGCTAGCCCTTTCTGAACACAGCCATC 851
Qy 841 AACTTCTTCTTACTGTCTTATCAGCAAGCGGTTCCGCAACATGGCAGCCGCGCACGCTC 900
Db 852 AACTTCTTCTTACTGTCTTATCAGCAAGCGGTTCCGCAACATGGCAGCCGCGCACGCTC 911
Qy 901 AAGGCTTTCTTCAAGTGCCAGAGCAACCTGTACAGTTCTTACCAATCATAACTTTTCC 960
Db 912 AAGGCTTTCTTCAAGTGCCAGAGCAACCTGTACAGTTCTTACCAATCATAACTTTTCC 971
Qy 961 ATAAACAGTAGCCCTTGGATCTCGCCGCAAACTCACACTGATCAAGATGCTGGGTAC 1020
Db 972 ATAAACAGTAGCCCTTGGATCTCGCCGCAAACTCACACTGATCAAGATGCTGGGTAC 1031
Qy 1021 CAGTATGACAAAATGAAAACCTATAAAAAGTGTAAATGACAGCAAAAAGCTCTTACCAG 1080
Db 1032 CAGTATGACAAAATGAAAACCTATAAAAAGTGTAAATGACAGCAAAAAGCTCTTACCAG 1091
Qy 1081 TTTGAGAGTGCCATTTGGAGCTTGTGTATCATCTCTGTGA 1119
Db 1092 TTTGAGAGTGCCATTTGGAGCTTGTGTATCATCTCTGTGA 1130

```
RESULT 6
US-10-314-076-1
; Sequence 1, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM34, AND VARIANTS A
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338,371
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1047)..(2162)
; OTHER INFORMATION:
US-10-314-076-1

Query Match      100.0%; Score 1119; DB 16; Length 2198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGAGCACAGCAGCCACCTCGCAGCCACAGCTCGCTGCTTGGTGGTCCCGGC 60
DB      1  ATGGAGCACAGCAGCCACCTCGCAGCCACAGCTCGCTGCTTGGTGGTCCCGGC 1106

QY      61  TCGGCTCGGGTTCGTCGCTGCTACTACAGCTCTTGTGCTGCTCGGT 120
DB      1107 TCGGCTCGGGTTCGTCGCTGCTACTACAGCTCTTGTGCTGCTCGGT 1166

QY      121 TTACAGCAAAATATCTGACAGTATCATCTCTCCAGCTGGTGGGAGAGACAGAAG 180
DB      1167 TTACAGCAAAATATCTGACAGTATCATCTCTCCAGCTGGTGGGAGAGACAGAAG 1226

QY      181 TCCTCTCAACTATCTCTTGGACCTCGCTGCTGGACATCTTGGTCTCTTTTCATA 240
DB      1227 TCCTCTCAACTATCTCTTGGACCTCGCTGCTGGACATCTTGGTCTCTTTTCATA 1286

QY      241 GTGTTGTGGACTTCTCTGTGGAAGATTTCATCTTGAACATGCAGATGCTCAGGTCCCC 300
DB      1287 GTGTTGTGGACTTCTCTGTGGAAGATTTCATCTTGAACATGCAGATGCTCAGGTCCCC 1346

QY      301 GACAGATCATAGAGTGTGGAATTCTCATCTCCACACTCCATATGGAATTACTGTA 360
DB      1347 GACAGATCATAGAGTGTGGAATTCTCATCTCCACACTCCATATGGAATTACTGTA 1406

QY      361 CGGTTAACTGACAGGTATATCGCTGCTGCGACCGCTCAAGTACACAGCTCTCA 420
DB      1407 CGGTTAACTGACAGGTATATCGCTGCTGCGACCGCTCAAGTACACAGCTCTCA 1466

QY      421 TACCCAGCCGACCCCGAAAGTCATTGTGAAGTGTTCATACCTGCTCTCTGACCAAGC 480
DB      1467 TACCCAGCCGACCCCGAAAGTCATTGTGAAGTGTTCATACCTGCTCTCTGACCAAGC 1526

QY      481 ATCCCTCTATTACTGTGGCCCAACATCTGGAAGTGAAGTACATCAGCACTCTGTGCAT 540
DB      1527 ATCCCTCTATTACTGTGGCCCAACATCTGGAAGTGAAGTACATCAGCACTCTGTGCAT 1586

QY      541 CAGCTCTCTATCTGATCCACTGCTTCAAGTCTACCTGCTGCTGCTGCTGCTGCTGCT 600
DB      1587 CAGCTCTCTATCTGATCCACTGCTTCAAGTCTACCTGCTGCTGCTGCTGCTGCTGCT 1646

QY      601 ATCTTGAACATCAATCATTTGTGTACAAAGCTCAGGAGGAGAGCAATTTTTCGTCTCCGTGGC 660
DB      1  ATCTTGAACATCAATCATTTGTGTACAAAGCTCAGGAGGAGAGCAATTTTTCGTCTCCGTGGC 1706

QY      661 TACTCCACGGGAGAGACACCGCCATCTTGTTCACCATTACCTTCATCTTTGCCACACTT 720
DB      1707 TACTCCACGGGAGAGACACCGCCATCTTGTTCACCATTACCTTCATCTTTGCCACACTT 1766

QY      721 TGGGCCCCCGGCATCATCATGATCTTTTACCACTCTATGGGGGCCCATCCAGAACCGC 780
DB      1767 TGGGCCCCCGGCATCATCATGATCTTTTACCACTCTATGGGGGCCCATCCAGAACCGC 1826

QY      781 TGGCTGTGTACACATCATGTCCGACATTCGCCAACATGCTAGCCCTTCTGAAACACAGCCATC 840
DB      1827 TGGCTGTGTACACATCATGTCCGACATTCGCCAACATGCTAGCCCTTCTGAAACACAGCCATC 1886

QY      841 AACTTCTTCTCTACTGCTTCATGCAAGGGGTTCCGACCATGCGAGCGCGCAGGCTC 900
DB      1887 AACTTCTTCTCTACTGCTTCATGCAAGGGGTTCCGACCATGCGAGCGCGCAGGCTC 1946

QY      901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTTCTACCAATCATAACTTTTCC 960
DB      1947 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTTCTACCAATCATAACTTTTCC 2006

QY      961 ATACAGATAGCCCTCGATCTCGCCGCAAACTCACACTGCATCAAGATGCTGGTGTAC 1020
DB      2007 ATACAGATAGCCCTCGATCTCGCCGCAAACTCACACTGCATCAAGATGCTGGTGTAC 2066

QY      1021 CAGTATGACAAAATGGAACCTATATAAAGTGTGTATGACAGCAAAAGCTCTCTACCAG 1080
DB      2067 CAGTATGACAAAATGGAACCTATATAAAGTGTGTATGACAGCAAAAGCTCTCTACCAG 2126

QY      1081 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGCA 1119
DB      2127 TTTGAAGATGCCATTGGAGCTTGTGTATCATCTCTGTGCA 2165

RESULT 7
US-10-314-076-3
; Sequence 3, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM34, AND VARIANTS A
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1107)
; OTHER INFORMATION:
US-10-314-076-3

Query Match      97.5%; Score 1091; DB 16; Length 1110;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1110; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY      1  ATGGAGCACAGCAGCCACCTCGCAGCCACAGCTCGCTGCTTGTGTTGGTGGTCCCGGC 60
DB      1  ATGGAGCACAGCAGCCACCTCGCAGCCACAGCTCGCTGCTTGTGTTGGTGGTCCCGGC 60

QY      61 TCGGCTCGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB      61 TCGGCTCGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY      121 TTACAGCAAAATATCTTGTGACAGTGTATCTCTCCAGCTGGTGGGAGAGACAGAAG 180
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Db 121 TTACCAAGCAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAAG 180
Qy 181 TCCTCTACAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTGTCTCTTTTCATA 240
Db 181 TCCTCTACAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTGTCTCTTTTCATA 240
Qy 241 GTGTTTGTGGACTCTCTTGTGGAAATTTTCATCTTGAACATGAGATGCTCAGGTCCCG 300
Db 241 GTGTTTGTGGACTCTCTTGTGGAAATTTTCATCTTGAACATGAGATGCTCAGGTCCCG 300
Qy 301 GACAAGATCATGAAGTCTGGAATTTCTCATCCATCCACACCTCCATATGGAATTAAGTGA 360
Db 301 GACAAGATCATGAAGTCTGGAATTTCTCATCCATCCACACCTCCATATGGAATTAAGTGA 360
Qy 361 CGGTTAACCAATTGACAGGTATATCGCTGCTGCGCACCCGCTCAAGTACCACACGGTCTCA 420
Db 361 CGGTTAACCAATTGACAGGTATATCGCTGCTGCGCACCCGCTCAAGTACCACACGGTCTCA 420
Qy 421 TACCCAGCCGGCAACCCGGAAAGTTCATGTAAGTGTTCATACACCTGCTTCTGACCAAGC 480
Db 421 TACCCAGCCGGCAACCCGGAAAGTTCATGTAAGTGTTCATACACCTGCTTCTGACCAAGC 480
Qy 481 ATCCCTATTTACTGTTGGCCCAACATCTGCACTGGAAGTATACATGACCACTCTGTGCAT 540
Db 481 ATCCCTATTTACTGTTGGCCCAACATCTGCACTGGAAGTATACATGACCACTCTGTGCAT 540
Qy 541 CAGCTCCTCATCTGGAATCACTGCTTCAACGCTTACCTGCTGCTGCTTCTTCTTTC 600
Db 541 CAGCTCCTCATCTGGAATCACTGCTTCAACGCTTACCTGCTGCTGCTTCTTCTTTC 600
Qy 601 ATCTGAACTCAATCATATGTTGTAACAAGCTCAGAGGAAGCAATTTTCTGCTCGTGGC 660
Db 601 ATCTGAACTCAATCATATGTTGTAACAAGCTCAGAGGAAGCAATTTTCTGCTCGTGGC 660
Qy 661 TACTCCACGGGGAAGACACCGCATCTTGTTCACCACTTACCTCCATCTTGGCACACTT 720
Db 661 TACTCCACGGGGAAGACACCGCATCTTGTTCACCACTTACCTCCATCTTGGCACACTT 720
Qy 721 TGGGCCCCCGCATCATGATTTCTTTACCACTCTATGCGGCGGCCCATCCAGAACCGC 780
Db 721 TGGGCCCCCGCATCATGATTTCTTTACCACTCTATGCGGCGGCCCATCCAGAACCGC 780
Qy 781 TGGCTGGTACACATCATGATTCGCAATTCGCAACATGCTAGCCCTTCTGAACACAGCCATC 840
Db 781 TGGCTGGTACACATCATGATTCGCAATTCGCAACATGCTAGCCCTTCTGAACACAGCCATC 840
Qy 841 AACTTCTTCTCTACTGCTTTCATCAGCAAGCGGTTCCGCAACCATGCGCAGCGCCAGCTC 900
Db 841 AACTTCTTCTCTACTGCTTTCATCAGCAAGCGGTTCCGCAACCATGCGCAGCGCCAGCTC 900
Qy 901 AAGGCTTCTTCAAGTGGCCAGAACCTGTACAGTTCTACACCAATCATAACTTTTCC 960
Db 901 AAGGCTTCTTCAAGTGGCCAGAACCTGTACAGTTCTACACCAATCATAACTTTTCC 960
Qy 961 ATAAACAAGTAGCCCTTGGATCTGCGCGCAAACTCACACTGCACTCAAGATGCTGGTGTAC 1020
Db 961 ATAAACAAGTAGCCCTTGGATCTGCGCGCAAACTCACACTGCACTCAAGATGCTGGTGTAC 1020
Qy 1021 CAGTATGACAAAATGGAACCTATAAAAGTGTGTAATGACGAAAGCTCTTACCCAG 1080
Db 1021 CAGTATGACAAAATGGAACCTATAAAAGTGTGTAATGACGAAAGCTCTTACCCAG 1080
Qy 1081 TTTGAAGATGCAATTTGGAGCTTGTGTCATCATCTCTGTA 1119
Db 1072 TTTGAAGATGCAATTTGGAGCTTGTGTCATCATCTCTGTA 1110
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RESULT 8

US-10-219-834-6

; Sequence 6, Application US/10219834

; Publication No. US20030096751A1

; GENERAL INFORMATION:

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; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE TH
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219,834
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313,658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 2189
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-219-834-6
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Query Match 97.5%; Score 1091; DB 14; Length 2189;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1110; Conservative 0; Mismatches 0; Indels 9; Gaps 1;
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Qy 1 ATGGAGCACACGACGCGCCACCTCGCAGCCACAGCTCGCTCTTGGTGGTCCCCGGC 60
Db 1047 ATGGAGCACACGACGCGCCACCTCGCAGCCACAGCTCGCTCTTGGTGGTCCCCGGC 1106
Qy 61 TCGGCTCGGCTTGGTTCGTCGCGTGGTCTACTACAGCTCTTGTCTGTGCTCGCTCGGT 120
Db 1107 TCGGCTCGGCTTGGTTCGTCGCGTGGTCTACTACAGCTCTTGTCTGTGCTCGGT 1166
Qy 121 TTACAGCAAAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAAG 180
Db 1167 TTACAGCAAAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAAG 1226
Qy 181 TCCTCTTACAACTATCTTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 240
Db 1227 TCCTCTTACAACTATCTTGGCACTCGCTGCTGCGGACATCTTGGTCTCTTTTTCATA 1286
Qy 241 GTGTTTGTGACTTCTCTGTTGGAAGATTTTCATCTTGAACATGAGATGCTCAGGTCCCC 300
Db 1287 GTGTTTGTGACTTCTCTGTTGGAAGATTTTCATCTTGAACATGAGATGCTCAGGTCCCC 1346
Qy 301 GACAAGATCATGAAGTCTGGAATTTCTCATCCATCCACCTCCATATGGAATTAAGTGA 360
Db 1347 GACAAGATCATGAAGTCTGGAATTTCTCATCCATCCACCTCCATATGGAATTAAGTGA 1406
Qy 361 CGGTTAACCAATTGACAGGTATATCGCTGCTGCCACCCGCTCAAGTACCACAGGTCTCA 420
Db 1407 CGGTTAACCAATTGACAGGTATATCGCTGCTGCCACCCGCTCAAGTACCACAGGTCTCA 1466
Qy 421 TACCCAGCCGGCAACCCGGAAAGTTCATGTAAGTGTTCATACACCTGCTTCTGACCAAGC 480
Db 1467 TACCCAGCCGGCAACCCGGAAAGTTCATGTAAGTGTTCATACACCTGCTTCTGACCAAGC 1526
Qy 481 ATCCCTATTTACTGTTGGCCCAACATCTGGAATGGAAGTATACATGACCACTCTGTGCAAT 540
Db 1527 ATCCCTATTTACTGTTGGCCCAACATCTGGAATGGAAGTATACATGACCACTCTGTGCAAT 1586
Qy 541 CAGCTCCTCATCTGGAATCACTGCTTCAACGCTTACCTGCTGCTGCTGCTGCTTCTTCTTC 600
Db 1587 CAGCTCCTCATCTGGAATCACTGCTTCAACGCTTACCTGCTGCTGCTGCTGCTTCTTCTTC 1646
Qy 601 ATCTTGAATCAATATTTGTGTACAGCTCAGGAGGAGCAATTTTCTGCTCCGTGGC 660
Db 1647 ATCTTGAATCAATATTTGTGTACAGCTCAGGAGGAGCAATTTTCTGCTCCGTGGC 1706
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QY 661 TACTCCAGGGAGACACACCGCCATCTTGTTACCACTTACCTCATCTTTGGCCACACTT 720
DB |||||
1707 TACTCCAGGGAGACACACCGCCATCTTGTTACCACTTACCTCATCTTTGGCCACACTT 1766
QY 721 TGGGCCCCCGCGCATCATCATGATCTTTTACCACTCTATGAGGGGCCCATCCAGAACCGC 780
DB |||||
1767 TGGGCCCCCGCGCATCATCATGATCTTTTACCACTCTATGAGGGGCCCATCCAGAACCGC 1826
QY 781 TGGGCTGTACACATCATCTCCGACATCTCCGACATCTGCTAGCCCTCTGAAACACAGCCATC 840
DB |||||
1827 TGGGCTGTACACATCATCTCCGACATCTCCGACATCTGCTAGCCCTCTGAAACACAGCCATC 1886
QY 841 AACTTCTTCTCTACTGCTTCTATCAGCAAGCGGTTCCGACCATGCGGAGCGCCACGCTC 900
DB |||||
1887 AACTTCTTCTCTACTGCTTCTATCAGCAAGCGGTTCCGACCATGCGGAGCGCCACGCTC 1946
QY 901 AAGGCTTTCTCAAGTGCAGAGCAACCTGTACAGTTCTACCAATCATPAACCTTTTCC 960
DB |||||
1947 AAGGCTTTCTCAAGTGCAGAGCAACCTGTACAGTTCTACCAATCATPAACCTTTTCC 2006
QY 961 ATACCAAGTAGCCCTGATCTCGCGGCAAACTCACTGATCAAGTCTGCTGTGTAC 1020
DB |||||
2007 ATACCAAGTAGCCCTGATCTCGCGGCAAACTCACTGATCAAGTCTGCTGTGTAC 2066
QY 1021 CAGTATGACAAAATGGAAACCTATAAAAGTCTGTAATGACAGCAAAAGCTCTTACCAG 1080
DB |||||
2067 CAGTATGACAAAATGG-----AAAAAGTCTGTAATGACAGCAAAAGCTCTTACCAG 2117
QY 1081 TTTGAAGATGCCATTTGGAGCTTGTGTATCATCTCTGTGA 1119
DB |||||
2118 TTTGAAGATGCCATTTGGAGCTTGTGTATCATCTCTGTGA 2156

RESULT 9

US-10-450-590-1
; Sequence 1, Application US/10450590
; Publication No. US20040076985A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN CHEMOKINE-LIKE RECEPTOR
; FILE REFERENCE: LIO316 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/450,590
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/254,923
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US 60/280,110
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/299,474
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-590-1

Query Match 93.8%; Score 1050; DB 17; Length 1059;
Best Local Similarity 100.0%; Pred. No. 7,3e-310;
Matches 1050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCACAGCAGCCACCTCGCAGCCACAGCTGCTTGTGCTCCCGGC 60
DB |||||
1 ATGGAGCACAGCAGCCACCTCGCAGCCACAGCTGCTTGTGCTCCCGGC 60
QY 61 TCGGCTCGGCTTGGGTTTGGTCCGCTGCTACTACAGCTCTTGTGCTCGGT 120
DB |||||
61 TCGGCTCGGCTTGGGTTTGGTCCGCTGCTACTACAGCTCTTGTGCTCGGT 120
QY 121 TTACAGCAAAATATTTGACAGTGTATCTCTCCAGCTGTTGGCAAGACAGAG 180
DB |||||
121 TTACAGCAAAATATTTGACAGTGTATCTCTCCAGCTGTTGGCAAGACAGAG 180

QY 181 TCCTCTACAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTTGGTCTCTTTTTCATA 240
DB |||||
181 TCCTCTACAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTTGGTCTCTTTTTCATA 240
QY 241 GTGTTTGTGACTTCTTGTGGAAGATTTCACTTTGAACATGCAAGATGCTCAGGTCCCC 300
DB |||||
241 GTGTTTGTGACTTCTTGTGGAAGATTTCACTTTGAACATGCAAGATGCTCAGGTCCCC 300
QY 301 GACAAGATCATAGAAGTCTGGAATTTCTATCCATCCACACCTCCATATGATGATGTA 360
DB |||||
301 GACAAGATCATAGAAGTCTGGAATTTCTATCCATCCACACCTCCATATGATGATGTA 360
QY 361 CCGTTAAACATTTGACAGATATATCGCTGTCTGCCACCGCTCAAGTACCAACCGTCTCA 420
DB |||||
361 CCGTTAAACATTTGACAGATATATCGCTGTCTGCCACCGCTCAAGTACCAACCGTCTCA 420
QY 421 TACCCAGCCCGCACCCCGGAAAGTCAATTGTAGTGTTTATCATCACTGCTCTCTGACCA 480
DB |||||
421 TACCCAGCCCGCACCCCGGAAAGTCAATTGTAGTGTTTATCATCACTGCTCTCTGACCA 480
QY 481 ATCCCTTACTTGTGTCGTCACCATCTGGACTGAAAGTACATCAGGACCTCTGTGCA 540
DB |||||
481 ATCCCTTACTTGTGTCGTCACCATCTGGACTGAAAGTACATCAGGACCTCTGTGCA 540
QY 541 CACGTCTCATCTGATCTCACTGCTTCAACCGTCTACCTGCTGCTCTCTCTCTCTTC 600
DB |||||
541 CACGTCTCATCTGATCTCACTGCTTCAACCGTCTACCTGCTGCTCTCTCTCTCTTC 600
QY 601 ATCTTGAACATCAATTTGTGTACAGCTCAGGAGGAGCAATTTTGTCTCCGTGGC 660
DB |||||
601 ATCTTGAACATCAATTTGTGTACAGCTCAGGAGGAGCAATTTTGTCTCCGTGGC 660
QY 661 TACTCCAGGGAGACACACCGCCATCTTGTTCACATTTACCTCCATCTTTGCCACACTT 720
DB |||||
661 TACTCCAGGGAGACACACCGCCATCTTGTTCACATTTACCTCCATCTTTGCCACACTT 720
QY 721 TGGGCCCCCGCGCATCATCATGATCTTTTACCACTCTATGAGGGGCCCATCCAGAACCGC 780
DB |||||
721 TGGGCCCCCGCGCATCATCATGATCTTTTACCACTCTATGAGGGGCCCATCCAGAACCGC 780
QY 781 TGGCTGTGTACATCATGTCCGACATTTGCCAATGCTAGCCCTTTCTGAACACAGCCATC 840
DB |||||
781 TGGCTGTGTACATCATGTCCGACATTTGCCAATGCTAGCCCTTTCTGAACACAGCCATC 840
QY 841 AACTTCTTCTTACTGCTTTCATCAGCAAGCGGTTCCGACCATGCGGAGCGCCACGCTC 900
DB |||||
841 AACTTCTTCTTACTGCTTTCATCAGCAAGCGGTTCCGACCATGCGGAGCGCCACGCTC 900
QY 901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCC 960
DB |||||
901 AAGGCTTTCTTCAAGTGCAGAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCC 960
QY 961 ATAAACAGTAGCCCTCGATCTCGCGGCAAACTCACACTGCTCAAGATGCTGGTGTAC 1020
DB |||||
961 ATAAACAGTAGCCCTCGATCTCGCGGCAAACTCACACTGCTCAAGATGCTGGTGTAC 1020
QY 1021 CAGTATGACAAAATGGAAACCTTATAAAA 1050
DB |||||
1021 CAGTATGACAAAATGGAAACCTTATAAAA 1050

RESULT 10

US-10-296-294A-3
; Sequence 3, Application US/10296294A
; Publication No. US20040029224A1
; GENERAL INFORMATION:
; APPLICANT: TERAOKA, Yasuko
; APPLICANT: MATSUI, Hideki
; APPLICANT: SHINTANI, Yabushi
; TITLE OF INVENTION: No. US20040029224A1el G Protein-Coupled Receptor and its DNA
; FILE REFERENCE: 2734 USOP
; CURRENT APPLICATION NUMBER: US/10/296,294A
; CURRENT FILING DATE: 2001-11-21

Query Match	93.8%;	Score 1050;	DB 14;	Length 1202;
Best Local Similarity	100.0%;	Pred. No. 7,8e-310;		
Matches 1050;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGAGCACACGACGCGCCACCTCGCAGCCAAACAGCTCGCTGCTCTTGGTGGTCCCGCGGC	60	
Db	68	ATGGAGCACACGACGCGCCACCTCGCAGCCAAACAGCTCGCTGCTCTTGGTGGTCCCGCGGC	127	
Qy	61	TCGGCCTCGCGCTTGGGTTCGCGCCGCTGCTCTACTACAGCCCTCTTGTCTGTGCTCGGT	120	
Db	128	TCGGCCTCGCGCTTGGGTTCGCGCCGCTGCTCTACTACAGCCCTCTTGTCTGTGCTCGGT	187	
Qy	121	TTACCAGCAAAATCTTGACAGTGATCATCCTCTCCCAGCTGGTGGCAAGAAGACAGAAAG	180	
Db	188	TTACCAGCAAAATCTTGACAGTGATCATCCTCTCCCAGCTGGTGGCAAGAAGACAGAAAG	247	
Qy	181	TCCTCTCTACAACATCTCTTTGGCAGCTCGCTGCTGCCGACATCTTTGGTCTCTTTTTTCATA	240	
Db	248	TCCTCTCTACAACATCTCTTTGGCAGCTCGCTGCTGCCGACATCTTTGGTCTCTTTTTTCATA	307	
Qy	241	GTGTTTGTGGACTTCCTGTTGGAGAATTCATCTTTGAACATGACAGATGCTCTCAGGTCCCC	300	
Db	308	GTGTTTGTGGACTTCCTGTTGGAGAATTCATCTTTGAACATGACAGATGCTCTCAGGTCCCC	367	

QY 301 GACAAAGATCATAGAAAGTCTGGAAATTCATCCATCCACACCTCCATATGATGACTGTA 360
Db |||||
QY 368 GACAAAGATCATAGAAAGTCTGGAAATTCATCCATCCACACCTCCATATGATGACTGTA 427
Db |||||
QY 361 CGGTTAAACATTGACAGGTATATCGTGTGCGCAACCGCTCAAGTACACACCGGTCTCA 420
Db |||||
QY 428 CGGTTAAACATTGACAGGTATATCGTGTGCGCAACCGCTCAAGTACACACCGGTCTCA 487
Db |||||
QY 421 TACCAGCCCGCACCGGAAAGTCAATGTAAGTGTTTACATCAGCACCTGCTCTGACACG 480
Db |||||
QY 488 TACCAGCCCGCACCGGAAAGTCAATGTAAGTGTTTACATCAGCACCTGCTCTGACACG 547
Db |||||
QY 481 ATCCCTCTATTACTGTGTGCGCAACATCTGGACTGAAGACTATACATCAGCACCTCTGTGCAT 540
Db |||||
QY 548 ATCCCTCTATTACTGTGTGCGCCAAATCTGACTGAAGACTATACATCAGCACCTCTGTGCAT 607
Db |||||
QY 541 CAGGTCCTCATCTGGATCCATGCTTCAACCGCTCACTGGTGGCCCTGCTCCATCTTCTTC 600
Db |||||
QY 608 CAGGTCCTCATCTGGATCCATGCTTCAACCGCTCACTGGTGGCCCTGCTCCATCTTCTTC 667
Db |||||
QY 601 ATCTTGAATCAATCATGTTGTATCAAGCTCAGGAGGAAGCAATTTTCGTCGCGTGC 660
Db |||||
QY 668 ATCTTGAATCAATCATGTTGTATCAAGCTCAGGAGGAAGCAATTTTCGTCGCGTGC 727
Db |||||
QY 661 TACTCCACGGGAAGACACCGCCATCTTGTTCACCATTTACTCTCCATCTTTGGCCACACTT 720
Db |||||
QY 728 TACTCCACGGGAAGACACCGCCATCTTGTTCACCATTTACTCTCCATCTTTGGCCACACTT 787
Db |||||
QY 721 TGGGCCCCCGCATCATCATGATTTCTTTACCACTCTATGGGGCGCCCATCCAGAACCGC 780
Db |||||
QY 788 TGGGCCCCCGCATCATCATGATTTCTTTACCACTCTATGGGGCGCCCATCCAGAACCGC 847
Db |||||
QY 781 TGGTGTGTACATCATGATCGGACATTTGCGCAACATGCTAGCCCTTCTGAACACAGCCATC 840
Db |||||
QY 848 TGGTGTGTACATCATGATCGGACATTTGCGCAACATGCTAGCCCTTCTGAACACAGCCATC 907
Db |||||
QY 841 AACTTCTTCTTCTACTGCTTCTATCAGCAAGCGTTTCGACCATGGCAGCGCCACAGCTC 900
Db |||||
QY 908 AACTTCTTCTTCTACTGCTTCTATCAGCAAGCGTTTCGACCATGGCAGCGCCACAGCTC 967
Db |||||
QY 901 AAGGCTTTCTTCAAGTGGCAGAACCTGTGTACAGTTCTACCAATATCAATCTTTTTC 960
Db |||||
QY 968 AAGGCTTTCTTCAAGTGGCAGAACCTGTGTACAGTTCTACCAATATCAATCTTTTTC 1027
Db |||||
QY 961 ATAAACAGTAGCCCTTGATCTCGCCGGCAAACTCAGCTGATCAAGATGCTGTGTATC 1020
Db |||||
QY 1028 ATAAACAGTAGCCCTTGATCTCGCCGGCAAACTCAGCTGATCAAGATGCTGTGTATC 1087
Db |||||
QY 1021 CAGTATGACAAAATGGAAACCTATAAAA 1050
Db |||||
QY 1088 CAGTATGACAAAATGGAAACCTATAAAA 1117
Db |||||

RESULT 12
US-09-995-225-15
; Sequence 15, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; PRIORITY FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-15

Query Match 93.7%; Score 1048.4; DB 9; Length 1062;
Best Local Similarity 99.9%; Pred. No. 2.3e-309;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGACACACGACGCGCCACCTCGACGCCAAACAGCTCGCTGTCTTGGTGTGTCGCCCGC 60
Db |||||
QY 1 ATGAGACACACGACGCGCCACCTCGACGCCAAACAGCTCGCTGTCTTGGTGTGTCGCCCGC 60
Db |||||
QY 61 TCGGCTCGGCTTGGGTTTGGTGGCTGTCTTACAGCCCTTGTCTGTGCTCGCTCGGT 120
Db |||||
QY 61 TCGGCTCGGCTTGGGTTTGGTGGCTGTCTTACAGCCCTTGTCTGTGCTCGGT 120
Db |||||
QY 121 TTACAGCAAAATATCTTGACAGTGTATCATCTCTCCAGCTGGGCAAGAGACAGAAAG 180
Db |||||
QY 121 TTACAGCAAAATATCTTGACAGTGTATCATCTCTCCAGCTGGGCAAGAGACAGAAAG 180
Db |||||
QY 181 TCCTCTCAAACTATCTCTTGGGCACTCGCTGTGCGGACATCTTGGTCTCTTTTTCATA 240
Db |||||
QY 181 TCCTCTCAAACTATCTCTTGGGCACTCGCTGTGCGGACATCTTGGTCTCTTTTTCATA 240
Db |||||
QY 241 GTGTTTGGGACTTCTGTTGGAGAGATTTCATCTTGAACATGACATGCTCAGGTGCCCC 300
Db |||||
QY 241 GTGTTTGGGACTTCTGTTGGAGAGATTTCATCTTGAACATGACATGCTCAGGTGCCCC 300
Db |||||
QY 301 GACAAGATCATAGAAAGTGTGGAATTCATCTCCATCCACACCTCCATATGATGACTGTA 360
Db |||||
QY 301 GACAAGATCATAGAAAGTGTGGAATTCATCTCCATCCACACCTCCATATGATGACTGTA 360
Db |||||
QY 361 CCGTTAAACATTGACAGGTATATCGTGTCTGCCACCGCTCAAGTACACACCGGTCTCA 420
Db |||||
QY 361 CCGTTAAACATTGACAGGTATATCGTGTCTGCCACCGCTCAAGTACACACCGGTCTCA 420
Db |||||
QY 421 TACCAGCCCGCACCGGAAAGTCAATGTAAGTGTTTACATCAGCACCTGCTCTGACACG 480
Db |||||
QY 421 TACCAGCCCGCACCGGAAAGTCAATGTAAGTGTTTACATCAGCACCTGCTCTGACACG 480
Db |||||
QY 481 ATCCCTCTATTACTGTGTGCGCCAAACATCTGGACTGAAGACTATACATCAGCACCTCTGTGCAT 540
Db |||||
QY 481 ATCCCTCTATTACTGTGTGCGCCAAACATCTGGACTGAAGACTATACATCAGCACCTCTGTGCAT 540
Db |||||
QY 541 CAGGTCCTCATCTGGATCCATGCTTCAACCGCTCACTGGTGGCCCTGCTCCATCTTCTTC 600
Db |||||
QY 541 CAGGTCCTCATCTGGATCCATGCTTCAACCGCTCACTGGTGGCCCTGCTCCATCTTCTTC 600
Db |||||

Qy	601	ATCTTGAACCTCAATCATTTGTGTACAGCTCAGAGGAGAGCAATTTTCCTCTCCGTGGC	660
Db	601	ATCTTGAACCTCAATCATTTGTGTACAGCTCAGAGGAGAGCAATTTTCCTCTCCGTGGC	660
Qy	661	TACTCCACGGGAGACACCGCATCTTGTTCACCAATACCTCCATCTTTGGCCACACTT	720
Db	661	TACTCCACGGGAGACACCGCATCTTGTTCACCAATACCTCCATCTTTGGCCACACTT	720
Qy	721	TGGGCCCCCGGCATCATCATGATTTCTTTACCACTCTATGGGGGGCCATCCAGAAACCGC	780
Db	721	TGGGCCCCCGGCATCATCATGATTTCTTTACCACTCTATGGGGGGCCATCCAGAAACCGC	780
Qy	781	TGGCTGTGTACATCATCTGCGACATTCGCAAGATGCTAGCCCTTCTGAACACAGGCATC	840
Db	781	TGGCTGTGTACATCATCTGCGACATTCGCAAGATGCTAGCCCTTCTGAACACAGGCATC	840
Qy	841	AACCTTCTCTCTACTGCTTTCATCAGCAAGCGGTTTCGCAACCATGCTAGCCCTTCTGAACACAGGCATC	900
Db	841	AACCTTCTCTCTACTGCTTTCATCAGCAAGCGGTTTCGCAACCATGCTAGCCCTTCTGAACACAGGCATC	900
Qy	901	AAGGCTTTCTTCAAGTGCCAGAGCAACCTGTACAGTTCTTACCAATCATTAACCTTTTCC	960
Db	901	AAGGCTTTCTTCAAGTGCCAGAGCAACCTGTACAGTTCTTACCAATCATTAACCTTTTCC	960
Qy	961	ATAACAAGTAGCCCTCGATCTCGCCGGCAAACTCACACTGCAATCAAGATGCTGGTGTAC	1020
Db	961	ATAACAAGTAGCCCTCGATCTCGCCGGCAAACTCACACTGCAATCAAGATGCTGGTGTAC	1020
Qy	1021	CAGTATGACAAAAAATGAAAAACCTATATAA	1050
Db	1021	CAGTATGACAAAAAATGAAAAACCTATATAA	1050

RESULT 13

US-09-995-225-15

Sequence 15, Application US/09995225

Publication No. US20030139588A9

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Chu, Zhi Liang

APPLICANT: Dang, Huang T.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Pride, Cameron

TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human C

TITLE OF INVENTION: Receptors

FILE REFERENCE: AREN-0308

CURRENT APPLICATION NUMBER: US/09/995,225

CURRENT FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: PCT/US99/23938

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/253,404

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/255,366

PRIOR FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: 60/270,286

PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 60/282,365

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/270,266

PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 60/282,032

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/282,358

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/282,356

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/290,917

PRIOR FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: 60/309,208

PRIOR FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 67

QY 901 AAGGCTTTCTCAAGTGCAGAGCAACCTGTACAGTTCTTACACCAATCATATACTTTTCC 960
DB |||||||
QY 901 AAGGCTTTCTCAAGTGCAGAGCAACCTGTACAGTTCTTACACCAATCATATACTTTTCC 960
DB |||||||
QY 961 ATAACAAGTAGCCCTGGATCTCGCCGCAAACTCACACTGATCAAGATGCTGGTGATC 1020
DB |||||||
QY 961 ATAACAAGTAGCCCTGGATCTCGCCGCAAACTCACACTGATCAAGATGCTGGTGATC 1020
DB |||||||
QY 1021 CAGTATGACAAAATGGAAAACCTTATAAA 1050
DB |||||||
QY 1021 CAGTATGACAAAATGGAAAACCTTATAAA 1050
DB |||||||

RESULT 14

US-10-296-294A-4
; Sequence 4, Application US/10296294A
; Publication No. US20040029224A1
; GENERAL INFORMATION:
; APPLICANT: MATSUI, Hideki
; APPLICANT: TERAU, Yasuko
; APPLICANT: SHINTANI, Yasushi
; TITLE OF INVENTION: No. US20040029224A1el G Protein-Coupled Receptor and its DNA
; FILE REFERENCE: 2734 USOP
; CURRENT APPLICATION NUMBER: US/10/296,294A
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: PCT/JP01/04643
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: JP 2000-170446
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: JP 2000-194926
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 4
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Human
US-10-296-294A-4

Query Match 93.7%; Score 1048.4; DB 17; Length 1062;
Best Local Similarity 99.9%; Pred. No. 2.3e-309;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGGACACAGCAGCCACCTCGCAGCAACAGCTCGCTGTCTTGGTGGTCCCGCGC 60
DB |||||||
QY 1 ATGAGGACACAGCAGCCACCTCGCAGCAACAGCTCGCTGTCTTGGTGGTCCCGCGC 60
DB |||||||
QY 61 TCGGCTCGGGCTTGGGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
DB |||||||
QY 121 TTACAGCAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAAG 180
DB |||||||
QY 121 TTACAGCAATATCTTGACAGTATCATCTCTCCAGCTGGTGGCAAGACAGAAG 180
DB |||||||
QY 181 TCCTCTCAACTATCTCTTGGCACTCGCTGTGCGGACATCTTGGTCTCTTTTTCATA 240
DB |||||||
QY 181 TCCTCTCAACTATCTCTTGGCACTCGCTGTGCGGACATCTTGGTCTCTTTTTCATA 240
DB |||||||
QY 241 GTGTTTGTGGACTTCTGTGTTGGAAGATTTCATCTTTGAAATGCAGATGCTCAGGTCCCC 300
DB |||||||
QY 301 GACAAGATCATAGAAGTGTGAATTCATCCATCCACCTCATATGATTAATCTGTA 360
DB |||||||
QY 301 GACAAGATCATAGAAGTGTGAATTCATCCATCCACCTCATATGATTAATCTGTA 360
DB |||||||
QY 361 CGTTTAAACATTGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACCACAGCTCTCA 420
DB |||||||
QY 361 CGTTTAAACATTGACAGGTATATCGCTGTCTGCCACCGCTCAAGTACCACAGCTCTCA 420
DB |||||||
QY 421 TACCCAGCCCGCACCAGGAAAGTCAATGTAGTGTATTACATCACCTGCTTCTGACACG 480
DB |||||||
QY 421 TACCCAGCCCGCACCAGGAAAGTCAATGTAGTGTATTACATCACCTGCTTCTGACACG 480
DB |||||||

QY 481 ATCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 540
DB |||||||
QY 481 ATCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCTGTGCAT 540
DB |||||||
QY 541 CACGTCTCATCTGGATCCACTGTCTTACCCGTCTACCTGTGGTGGTGGTGGTGGTGGTGGT 600
DB |||||||
QY 541 CACGTCTCATCTGGATCCACTGTCTTACCCGTCTACCTGTGGTGGTGGTGGTGGTGGTGGT 600
DB |||||||
QY 601 ATCTTGAATCAATCATCTGTTGTAAGCTCAGGAGGAAGAGCAATTTTTCGTCTCGTGGC 660
DB |||||||
QY 601 ATCTTGAATCAATCATCTGTTGTAAGCTCAGGAGGAAGAGCAATTTTTCGTCTCGTGGC 660
DB |||||||
QY 661 TACTCCAGGGGAGAGCACCGCCCATCTTGTTCACCAATACCTCCATCTTTGCCACACTT 720
DB |||||||
QY 661 TACTCCAGGGGAGAGCACCGCCCATCTTGTTCACCAATACCTCCATCTTTGCCACACTT 720
DB |||||||
QY 721 TGGGCCCCCGCATCATCATGATTTCTTTACCACTCTATGGGGGGCCCATCCAGAACCGC 780
DB |||||||
QY 721 TGGGCCCCCGCATCATCATGATTTCTTTACCACTCTATGGGGGGCCCATCCAGAACCGC 780
DB |||||||
QY 781 TGGTGGTGTACATCATCTGTCCGACATTTGCCAAACATGTAGCCCTTCTGAAACACAGCCATC 840
DB |||||||
QY 781 TGGTGGTGTACATCATCTGTCCGACATTTGCCAAACATGTAGCCCTTCTGAAACACAGCCATC 840
DB |||||||
QY 841 AACTTCTTCTCTACTCTTCTCATCAGCAAGCGGTTCCGACCATGGCAGCGCCGACGCTC 900
DB |||||||
QY 841 AACTTCTTCTCTACTCTTCTCATCAGCAAGCGGTTCCGACCATGGCAGCGCCGACGCTC 900
DB |||||||
QY 901 AAGGCTTTCTTCAAGTGCAGAACCTGTACAGTTCTTACACCAATCATATACTTTTCC 960
DB |||||||
QY 901 AAGGCTTTCTTCAAGTGCAGAACCTGTACAGTTCTTACACCAATCATATACTTTTCC 960
DB |||||||
QY 961 ATAAACAAGTAGCCCTGGATCTCGCCGCAAACTCACACTGATCAAGATGCTGGTGATC 1020
DB |||||||
QY 961 ATAAACAAGTAGCCCTGGATCTCGCCGCAAACTCACACTGATCAAGATGCTGGTGATC 1020
DB |||||||
QY 1021 CAGTATGACAAAATGGAAAACCTTATAAA 1050
DB |||||||
QY 1021 CAGTATGACAAAATGGAAAACCTTATAAA 1050
DB |||||||

RESULT 15

US-09-813-432-21
; Sequence 21, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28

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